

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2003, 08:32:46 ; Search time 207.841 Seconds

(without alignments)
8065.662 Million cell updates/sec

Title: US-08-951-733-19

Perfect score: 3798

Sequence: 1 CCACGCTCGGGCAGCGCT.....GGAATAGTCATCCCTGAT 3798

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 3784.4 | 99.6 | 4015 | 3 | US-08-974-549A-1 |
| 3 | 3784.4 | 99.6 | 4015 | 3 | US-08-854-050-224 |
| 4 | 3784.4 | 99.6 | 4015 | 4 | US-09-430-323-224 |
| 5 | 3784.4 | 99.6 | 4015 | 4 | US-09-572-423B-3 |
| 6 | 3784.4 | 99.6 | 4015 | 4 | US-09-128-354-1 |
| 7 | 3784.4 | 99.6 | 4015 | 4 | US-09-675-321-1 |
| 8 | 3784.4 | 99.6 | 4015 | 4 | US-09-052-919-1 |
| 9 | 3784.4 | 99.6 | 4015 | 4 | US-08-912-951-1 |
| 10 | 3784.4 | 99.6 | 4015 | 4 | US-09-733-294A-3 |
| 11 | 3779.2 | 99.5 | 4037 | 3 | US-08-974-549A-343 |
| 12 | 3618.6 | 95.3 | 4029 | 3 | US-08-851-843A-173 |
| 13 | 3618.6 | 95.3 | 4029 | 3 | US-08-974-549A-292 |
| 14 | 3618.6 | 95.3 | 4029 | 3 | US-08-854-050-173 |
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| 19 | 2200.8 | 57.9 | 3396 | 3 | US-08-974-549A-639 |
| 20 | 2196.6 | 57.8 | 3396 | 3 | US-08-974-549A-638 |
| 21 | 1862.2 | 49.0 | 3396 | 3 | US-08-974-549A-642 |
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ALIGNMENTS

RESULT 1

US-08-851-843A-224
; Sequence 224, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/851.843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:

Sequence 100, App
Sequence 640, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 30, Appl
Sequence 62, Appl
Sequence 8, Appli
Sequence 62, Appl
Sequence 31, Appl
Sequence 9, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 11, Appl
Sequence 697, App

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|---------------------------|-----------------|--|-------------------|--------------|--|
| SEQUENCE CHARACTERISTICS: | | | | | |
| : LENGTH: | 4015 base pairs | | | | |
| : TYPE: | nucleic acid | | | | |
| : STRANDEDNESS: | single | | | | |
| : TOPOLOGY: | linear | | | | |
| : MOLECULE TYPE: | CDNA | | | | |
| : FEATURE: | | | | | |
| : NAME/KEY: | CDS | /product= "hprt" | | | |
| : LOCATION: | 56..3454 | /note= "human telomerase reverse | | | |
| : OTHER INFORMATION: | | transcriptase (hprt) | catalytic protein | | |
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| US-08-851-843A-224 | | | | | |
| Query Match | 99.6%; | Score 3784.4; | DB 3; | Length 4015; | |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | | |
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| Qy | 13 | GCAGCGCTGCTTCCTGTGCGCACAGTGGGAAGCCCTGCCCCCACCGATGCC | 72 | | |
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| Qy | 73 | CGCGCTCCCCGCTGCGGAGCCGTCGCTCCCTGCTGGGAGCACCATTACCGAGGTGCT | 132 | | |
| Dd | 61 | CGCGCTCCCCGCTGCGGAGCCGTCGCTCCCTGCTGGGAGCACCATTACCGAGGTGCT | 120 | | |
| Qy | 133 | GCGCTTGCCACAGTTTCGTGGCGGCCCTGGGGCCCCAGGGCTGGGGCTGGTGACGCGGG | 192 | | |
| Dd | 121 | GCGCTTGCCACAGTTTCGTGGCGGCCCTGGGGCCCCAGGGCTGGGGCTGGTGACGCGGG | 180 | | |
| Qy | 193 | GGACCCGGCGGCTTTCGCGCGCGCTGGTGCCCACTGCTGCTGGTGCCTGGGAGCGC | 252 | | |
| Dd | 181 | GGACCCGGCGGCTTTCGCGCGCGCTGGTGCCCACTGCTGCTGGTGCCTGGGAGCGC | 240 | | |
| Qy | 253 | ACGGCCGGCCCCCGCGGCCCTCCTTCCGCCAGGTGTCTTGCCTGAAGAGACTGGTGGC | 312 | | |
| Dd | 241 | ACGGCCGGCCCCCGCGGCCCTCCTTCCGCCAGGTGTCTTCCGCCAGGTGTCTTGAAGAGACTGGTGGC | 300 | | |
| Qy | 313 | CCGAGTGTGCAGAGGCTGTGCGAGCGGGCGCGAAGAAGCTGTGGCTTTCGGCTTCGC | 372 | | |
| Dd | 301 | CCGAGTGTGCAGAGGCTGTGCGAGCGGGCGCGAAGAAGCTGTGGCTTTCGGCTTCGC | 360 | | |
| Qy | 373 | GCTGCTGGACGGGGCCCGCGGGGCCCCCCCGAGGCCCTTACCACAGCTGCGCAGCTA | 432 | | |
| Dd | 361 | GCTGCTGGACGGGGCCCGCGGGGCCCCCCCGAGGCCCTTACCACAGCTGCGCAGCTA | 420 | | |
| Qy | 433 | CTTGCCCAACAGGTGACCGACGACATGCGGGGGAGCGGGGGCTGCTGCTGCG | 492 | | |
| Dd | 421 | CTTGCCCAACAGGTGACCGACGACATGCGGGGGAGCGGGGGCTGCTGCTGCG | 480 | | |
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| Dd | 481 | CCGGTGGGCGACACAGTGTCTGTTCACCTGCTGSCAGCTGCGGCGCTTTTGTGCTGCT | 540 | | |
| Qy | 553 | GGCTCCAGCTGCGCCTACCAAGTGTGCGGGCCCGCGCTGTACCAGCTCGCGCTGCCAC | 612 | | |
| Dd | 541 | GGCTCCAGCTGCGCCTACCAAGTGTGCGGGCCCGCGCTGTACCAGCTCGCGCTGCCAC | 600 | | |
| Qy | 613 | TCAGGCCGGGCCCCCGCCACACGCTAGTGTGACCCCGAAGGCGCTTGGGATGCGAACGGGC | 672 | | |
| Dd | 601 | TCAGGCCGGGCCCCCGCCACACGCTAGTGTGACCCCGAAGGCGCTTGGGATGCGAACGGGC | 660 | | |
| Qy | 673 | CTTGAACCATAGCTCAGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCGGGTGCAG | 732 | | |
| Dd | 661 | CTTGAACCATAGCTCAGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCGGGTGCAG | 720 | | |
| Qy | 733 | GAGCGGGGGGCAAGTGCCAGCCGAAGTCTCCGCTTGCCCAAGAGGCCACAGCGTGGCG | 792 | | |
| Dd | 721 | GAGCGGGGGGCAAGTGCCAGCCGAAGTCTCCGCTTGCCCAAGAGGCCACAGCGTGGCG | 780 | | |
| Qy | 793 | TGCCCTGAGCGGAGGGAGCGCCCTTGGGAGGGGTCTTGGGCCCCACCGGGGAGGAC | 852 | | |

;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/974,549A
;; FILING DATE: 19-NOV-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4015 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 56..3454
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;; OTHER INFORMATION: /note= "human telomerase reverse
;; OTHER INFORMATION: transcriptase (hTRT) catalytic protein
;; OTHER INFORMATION: component"
US-08-974-549A-1

Query Match 99.6%; Score 3784.4; DB 3; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GCAGCGTGGCTCTGCTGGCAGCTGGGAGCCCTGGCCCCGGCCACCCCGCGGATGCC 72
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| 133 | GCGCGTGGCAGCTTCTGCTGGCGGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGGG 192 |
| 121 | GCGCGTGGCCACGTTCTGCTGGCGGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGGG 180 |
| 193 | GGACCCGGCGCTTTCGCGGCTGGTGGCCAGTGGCTGGCTGGCTGGCTGGCTGGCTGG 252 |
| 181 | GGACCCGGCGCTTTCGCGGCTGGTGGCCAGTGGCTGGCTGGCTGGCTGGCTGGCTGG 240 |
| 253 | ACGGCGGCCCCCGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 312 |
| 241 | ACGGCGGCCCCCGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 300 |
| 313 | CGGAGTGTGAGAGGCTGTGCGAGCGGCGGCGGCGGAGAACGTGCTGGCTGGCTGG 372 |
| 301 | CGGAGTGTGAGAGGCTGTGCGAGCGGCGGCGGCGGAGAACGTGCTGGCTGGCTGG 360 |
| 373 | GCTGCTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 432 |
| 361 | GCTGCTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420 |
| 433 | CGTGGCCAAACAGCGTGACGAGCGCTGCGGGGAGCGGGCGGCTGGCTGGCTGG 492 |
| 421 | CGTGGCCAAACAGCGTGACGAGCGCTGCGGGGAGCGGGCGGCTGGCTGGCTGG 480 |
| 493 | CGGCGTGGCGGAGAGCGTGTGCTGGTTCACCTGCTGGGAGCGCTGGCGCTGGTGTGT 552 |
| 481 | CGGCGTGGCGGAGAGCGTGTGCTGGTTCACCTGCTGGGAGCGCTGGCGCTGGTGTGT 540 |
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| 793 | TGCCCCCTGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 852 |
| 781 | TGCCCCCTGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840 |
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| 913 | CACCTCTTTTGGAGGCTGCGCTCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCG 972 |
| 901 | CACCTCTTTTGGAGGCTGCGCTCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCG 960 |
| 973 | GCACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1032 |
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| | | | |
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| Db | 1141 | GACCATCTTTCTGGTTCCAGGCTTGGATGCCAGGACTCCCGCAGGTTGCCCCGGCT | 1200 |
| QY | 1213 | GCCCCAGCGTACTTGGCAAAATGCGGCCCTCTGTTTCTGGAGTGTCTTGGGAACCAACGCGCA | 1272 |
| Db | 1201 | GCCCCAGCGTACTTGGCAAAATGCGGCCCTCTGTTTCTGGAGTGTCTTGGGAACCAACGCGCA | 1260 |
| QY | 1273 | GTGCCCCCTACGGGTGTCTCTCAAGACGACTGCCCGCTGGAGTGTGGGTACCCGACG | 1332 |
| Db | 1261 | GTGCCCCCTACGGGTGTCTCTCAAGACGACTGCCCGCTGGAGTGTGGGTACCCGACG | 1320 |
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| Db | 1321 | AGCGGTGTCTGTCCCGGAGAACCCAGGGCTCTGTGCGGCCCGCCAGGAGGAGGA | 1380 |
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| Db | 1381 | CACAGACCCCGCTGCGCTGTGTGACGTGCTCCGCGACACAGACGCCCTTGGCAGGTGA | 1440 |
| QY | 1453 | CGGCTTCTGCGGGGCTGCTCTGCGCGGCTGGTGCCCGCAGGCTCTGCGGCTCCAGGCA | 1512 |
| Db | 1441 | CGGCTTCTGCGGGGCTGCTCTGCGCGGCTGGTGCCCGCAGGCTCTGCGGCTCCAGGCA | 1500 |
| QY | 1513 | CAAGAACCGGCTTCTCAGGACACCAAGAGTTTCTCTCTGGGGAGCATGCAAA | 1572 |
| Db | 1501 | CAAGAACCGGCTTCTCAGGACACCAAGAGTTTCTCTCTGGGGAGCATGCAAA | 1560 |
| QY | 1573 | GCTCTCGCTCAGGAGTGTGAGTGGAAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAG | 1632 |
| Db | 1561 | GCTCTCGCTCAGGAGTGTGAGTGGAAAGATGAGCGTGGGACTGCGCTTGGCTGCGCAG | 1620 |
| QY | 1633 | GAGCCAGGGGTGGCTGTGTCTGCGCGCGCAGACACCGTCTGCGTGAGGAGTCTGGC | 1692 |
| Db | 1621 | GAGCCAGGGGTGGCTGTGTCTGCGCGCGCAGACACCGTCTGCGTGAGGAGTCTGGC | 1680 |
| QY | 1693 | CAAGTCTCTGACGTGTGATGAGTGTGACGTGCTGAGTGTGCTGAGTGTCTTCTTTTA | 1752 |
| Db | 1681 | CAAGTCTCTGACGTGTGATGAGTGTGACGTGCTGAGTGTGCTGAGTGTCTTCTTTTA | 1740 |
| QY | 1753 | TGTACGGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAG | 1812 |
| Db | 1741 | TGTACGGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAG | 1800 |
| QY | 1813 | CAAGTTCCAAAGCATTTGGATCAGACAGACACTTGAAGAGGTGCAGTCTGGGAGCTGT | 1872 |
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| QY | 1873 | GGAAGCAGAGTTCAGGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCG | 1932 |
| Db | 1861 | GGAAGCAGAGTTCAGGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCG | 1920 |
| QY | 1933 | CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACGTACGTCGTGGAGC | 1992 |
| Db | 1921 | CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACGTACGTCGTGGAGC | 1980 |
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| Db | 1981 | CAGAACCTTCCGAGAGAAAGAGGCCGCGAGCGTCTCACCTTCGAGGTGAAGGCACTGTT | 2040 |
| QY | 2053 | CAGGCTCTCACTACAGGGGCGCGGCCCGCCCGGCTCTGCGGCCCTCTGTGTGGG | 2112 |
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| QY | 2113 | CTTGGAGCATATCCACAGGCGCTGGCGACCTTCTGCTGTGCTGGGCGCCAGGACCC | 2172 |
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| QY | 2473 | CAGTGGGCTCTTTCAGACCTCTTCTTACGTTTATGTCACACCGCTGCGCATCAGGG | 2532 |
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| QY | 2533 | CAAGTCTTACGTCCAGTGCCAGGGATGCCGAGGGTCTCATCTCTCCAGCTGCTCTG | 2592 |
| Db | 2521 | CAAGTCTTACGTCCAGTGCCAGGGATGCCGAGGGTCTCATCTCTCCAGCTGCTCTG | 2580 |
| QY | 2593 | CAGCTCTGCTTACGCGCACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCT | 2652 |
| Db | 2581 | CAGCTCTGCTTACGCGCACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCT | 2640 |
| QY | 2653 | GCTCTCGCTTGGTGGATGATTTCTTGTGGTGACACTCACCTCACCGCGGAAAC | 2712 |
| Db | 2641 | GCTCTCGCTTGGTGGATGATTTCTTGTGGTGACACTCACCTCACCGCGGAAAC | 2700 |
| QY | 2713 | CTTCTCTCAGGACCTGCTGCGAGGTGCCCTGAGTATGGCTGCGTGGTGAATTCGCGAA | 2772 |
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Db 3781 CCAGAT 3786

RESULT 3

US-08-854-050-224
; Sequence 224, Application US/08854050
; Patent No. 6261836

GENERAL INFORMATION:

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TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: PatentIn
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hprt"
OTHER INFORMATION: /note= "human telomerase reverse
OTHER INFORMATION: transcriptase (hTERT) catalytic protein
OTHER INFORMATION: component"
US-08-854-050-224

Query Match 99.6%; Score 3784.4; DB 3; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 361 GCTGCTGAGCGGGGCG 420
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| | Query Match | 98.6% | Score 3784..4; | DB 4; Length 4015; |
| | Best Local Similarity | 100.0%; | Pred. No. 0; | |
| | Matches 3785; Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| QY | 13 GCAGCGCTGGTGTCCTGCTGTGCACGTGGGAAGCCTTGGCCGCCCAATCCC | CGCATGCC | 72 | |
| Dd | 1 GCAGCGCTGGTGTCCTGCTGTGCACGTGGGAAGCCTTGGCCGCCCAATCCC | CGCATGCC | 60 | |

Db 2221 GACAGAGGCTACGGAGGTCATCGCAGCATCATCAAAACCCAGAACAGTACTGCGTGG 2280
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Db 2281 TCGGTATGCGGTGTCGCAAGAGCGCCATGCGGACAGTCCGCAAGGCTTCAAGAGCCA 2340
QY 2353 CGTCTCTACCTTACGACAGCTCCAGCGGTACATGCGACAGTTCGTGGCTACCTCAGGA 2412
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QY 2413 GACAGAGCGGTGAGGATGCGGTGTCATCGAGCAGAGCTCCCTCGATGATGAGGCGAG 2472
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QY 2473 CAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCCACAGCGCTGCCATCAGGG 2532
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QY 2533 CAACTCTACGTCAGTCCAGGGATCCCGAGGGCTCCATCTCTCCAGCTGCTCTG 2592
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Db 2641 GCTCTGCGTGTGGTGGATGATTTCTGTTGTGACACCTCACCTCACCCAGCGGAAAC 2700
QY 2713 CTTCTCAGGACCTGTCGAGGTGTCCTGAGTATGCGTGGTGAATTCGGA 2772
Db 2701 CTTCTCAGGACCTGTCGAGGTGTCCTGAGTATGCGTGGTGAATTCGGA 2760
QY 2773 GACAGTGTGACTTCCTGTAGAGAGAGGCGCTGGTGGCAGCGCTTTGTTGAGAT 2832
Db 2761 GACAGTGTGACTTCCTGTAGAGAGAGGCGCTGGTGGCAGCGCTTTGTTGAGAT 2820
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QY 2893 GCAGAGGACTACTCCAGTATGCGGACCTCCATCAGAGCGCTCAGCTTCAACGG 2952
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QY 2953 CCGCTTCAAGGCTGGAGAGACATGCTGCGAACTCTTTGGGCTTGGCGCTGAAGTG 3012
Db 2941 CCGCTTCAAGGCTGGAGAGACATGCTGCGAACTCTTTGGGCTTGGCGCTGAAGTG 3000
QY 3013 TCACAGCCTGTTCTGGATTTGAGGTGAACAGCGCTCCAGAGCGTGTGCACCAACATCTA 3072
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QY 3073 CAAAGATCCTCTGCTGAGGCGGTACAGGTTTCACGATGCTGCTGAGCTCCCATTTCA 3132
Db 3061 CAAAGATCCTCTGCTGAGGCGGTACAGGTTTCACGATGCTGCTGAGCTCCCATTTCA 3120
QY 3133 TCAGCAAGTTTGGAGAACCCACATTTTCTGCGCTCATCTCTGACAGCGCTCCCT 3192
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QY 3193 CTGCTACTCCATCTTGAAGCAAGAGCGGATGCTGCTGGGGGCAAGGGCGCGC 3252
Db 3181 CTGCTACTCCATCTTGAAGCAAGAGCGGATGCTGCTGGGGGCAAGGGCGCGC 3240
QY 3253 CCGGCGCTCTGCGCTCCGAGGCGGTGCAATGCTGTCACCAAGCATTTCTGCTCAAGT 3312
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Db 3301 GACTCGACACCGTGTACCTAGTGTCCACTCTCTGGGGTCACTCAGGACAGCGCCAGCA 3360
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Db 3361 GCTGAGTGGAAAGCTCCGCGGACAGCGTGTGCTGCTGGAGCGCGCAGCAACCGGC 3420
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QY 3493 GAGCAGACACAGAGCGCTGTACGCGGGCTCTACGTCCAGGAGGAGGGGGCGC 3552
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QY 3553 CACACCCAGGCGCCAGCGCTGGAGTCTGAGGCTGTAGTGTGTTTGGCGGAGCGCTG 3612
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QY 3613 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT 3672
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT 3660
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QY 3793 CCGTAT 3798
Db 3781 CCAGAT 3786

RESULT 5

US-09-572-423B-3
; Sequence 3, Application US/09572423B
; Patent No. 6331399
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William A. Gaarde
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0462
; CURRENT APPLICATION NUMBER: US/09/572,423B
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-572-423B-3

Query Match 99.6%; Score 3784.4; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GCAGCGCTGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCGGCGCACCCCGCGATGCC 72
Db 1 GCAGCGCTGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCGGCGCACCCCGCGATGCC 60
QY 73 GCGCGTCCCGCTGCGGAGCGTGGCTCCTGTGTGCGCAGCAGCTACCGGAGTGT 132
Db 61 GCGCGTCCCGCTGCGGAGCGTGGCTCCTGTGTGCGCAGCAGCTACCGGAGTGT 120
QY 133 GCGCGTGGCAGCTTGTGCGGCGCTGGGGCGCCCGCAGGCTGGCGCTGTCAGCGCG 192
Db 121 GCGCGTGGCAGCTTGTGCGGCGCTGGGGCGCCCGCAGGCTGGCGCTGTCAGCGCG 180

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|----|------|--|------|
| Qy | 193 | GGACCCGGCGGCTTTCGCGCGCTGTGTGGCCAGTGTGCTGTGTGTGTGCTGTGGAGCTGGACGC | 255 |
| Db | 181 | GGACCCGGCGGCTTTCGCGCGCTGTGTGGCCAGTGTGCTGTGTGTGTGCTGTGGAGCTGGACGC | 240 |
| Qy | 253 | ACGGCGCCCGCCGCGCGCCCTCTCTTCGCCAGGTGTCTGCTGTGAAGAGCTGTGGC | 312 |
| Db | 241 | ACGGCGCCCGCCGCGCGCCCTCTCTTCGCCAGGTGTCTGCTGTGAAGAGCTGTGGC | 300 |
| Qy | 313 | CCGAGTGTCTGCAGAGGTGTTCGAGCGCGCGCGAAGAGCTGTGCGCTTTCGGCTTTCGC | 372 |
| Db | 301 | CCGAGTGTCTGCAGAGGTGTTCGAGCGCGCGCGAAGAGCTGTGCGCTTTCGGCTTTCGC | 360 |
| Qy | 373 | GCTGCTGGACGGGGCCCGGGGGCCCGCCGAGGCCCTTCACACACAGCTGTGCGCAGCTA | 432 |
| Db | 361 | GCTGCTGGACGGGGCCCGGGGGCCCGCCGAGGCCCTTCACACACAGCTGTGCGCAGCTA | 420 |
| Qy | 433 | CCTGCCAACAACGGTGTACGACGACGTGCGGGGAGCGGGGCGGTGTGGGCTGTGCTGCG | 492 |
| Db | 421 | CCTGCCAACAACGGTGTACGACGACGTGCGGGGAGCGGGGCGGTGTGCTGCTGCG | 480 |
| Qy | 493 | CCGCGTGGGCGACAGCTGTGTGTTACCTGTCTGGCACGCTGCGCGCTCTTTTGTGCTGGT | 552 |
| Db | 481 | CCGCGTGGGCGACAGCTGTGTGTTACCTGTCTGGCACGCTGCGCGCTCTTTTGTGCTGGT | 540 |
| Qy | 553 | GGCTCCAGCTGTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGTGCGCGTGTCCAC | 612 |
| Db | 541 | GGCTCCAGCTGTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGTGCGCGTGTCCAC | 600 |
| Qy | 613 | TCAGGGCCCGCCCGCCACACGCTACTGTGACCCCGAAGCGTCTGGGATGCGAAGCGGC | 672 |
| Db | 601 | TCAGGGCCCGCCCGCCACACGCTACTGTGACCCCGAAGCGTCTGGGATGCGAAGCGGC | 660 |
| Qy | 673 | CTGGAACCATAGCTCAGGAGGCGGGGTCCCGCTGGGCTGTCCAGCCCGGGTGTGCGAG | 732 |
| Db | 661 | CTGGAACCATAGCTCAGGAGGCGGGGTCCCGCTGGGCTGTCCAGCCCGGGTGTGCGAG | 720 |
| Qy | 733 | GAGCGGGGGGAGTGCACCGAAGTGTGCGGTTGCCAAGAGGCCACAGGCGTGTGCGC | 792 |
| Db | 721 | GAGCGGGGGGAGTGCACCGAAGTGTGCGGTTGCCAAGAGGCCACAGGCGTGTGCGC | 780 |
| Qy | 793 | TGCCCTTAGCGGAGCGGACGCCGTGTGGCAGGGGTCTTGGGCCACCCGGCAGGAC | 852 |
| Db | 781 | TGCCCTTAGCGGAGCGGACGCCGTGTGGCAGGGGTCTTGGGCCACCCGGCAGGAC | 840 |
| Qy | 853 | GCGTGGACGAGTGACCGTGGTTCCTGTGTGTGTGTCACTTCCACAGACCCGCCAAGAAGC | 912 |
| Db | 841 | GCGTGGACGAGTGACCGTGGTTCCTGTGTGTGTGTCACTTCCACAGACCCGCCAAGAAGC | 900 |
| Qy | 913 | CACCTCTTTGGAGGTGGCTCTCTGTGCAGCGGCACCTCCACCATCTGTGGGCGGCCA | 972 |
| Db | 901 | CACCTCTTTGGAGGTGGCTCTCTGTGCAGCGGCACCTCCACCATCTGTGGGCGGCCA | 960 |
| Qy | 973 | GCACAGCGGGCCCCCATCCACATCGCGGCACACAGTCCCTTGGGACACGCTTGTCC | 1032 |
| Db | 961 | GCACAGCGGGCCCCCATCCACATCGCGGCACACAGTCCCTTGGGACACGCTTGTCC | 1020 |
| Qy | 1033 | CCCGGTGTACCGGAGACCAAGCACTTCTCTACTCTCTAGGGGACAAAGGAGCAGTGTGC | 1092 |
| Db | 1021 | CCCGGTGTGTACCGGAGACCAAGCACTTCTCTACTCTCTAGGGGACAAAGGAGCAGTGTGC | 1080 |
| Qy | 1093 | GCCCTCTCTCTACTAGCTCTCTGAGGCCACAGCTGACTGTGGCGCTCGGAGGCTGTGGA | 1152 |
| Db | 1081 | GCCCTCTCTCTACTAGCTCTCTGAGGCCACAGCTGACTGTGGCGCTCGGAGGCTGTGGA | 1140 |
| Qy | 1153 | GACCATCTTTCTGGGTTCAGGCCCTTGGATGCCAGGACTTCCCGCAGGTTGCCCGCCT | 1212 |
| Db | 1141 | GACCATCTTTCTGGGTTCAGGCCCTTGGATGCCAGGACTTCCCGCAGGTTGCCCGCCT | 1200 |
| Qy | 1213 | GCCCCAGCGTACTTGGCAAAATGGGCCCTGTCTTCTGTGAGCTGTCTTGGGAACACAGCGCA | 1272 |
| Db | 1201 | GCCCCAGCGTACTTGGCAAAATGGGCCCTGTCTTCTGTGAGCTGTCTTGGGAACACAGCGCA | 1260 |
| Qy | 1273 | GTGCCCTTACGGGGTGTCTCTCAAGACGCACTGCCCGCTCGGAGCTGTGCTACCCAGC | 1332 |

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|----|------|--|---|------|
| Db | 1361 | | GTGCCCTACGGGGTGCTCCTCAAGACGACTGCCCGTGCAGCTCGGGTCACCCAGC | 1320 |
| Qy | 1333 | AGCCGGTGCTGTGCCCGGAGAACCCACAGGCTCTGTGCGGCCCGGAGGAGGA | 1392 | |
| Db | 1321 | AGCCGGTGCTGTGCCCGGAGAACCCACAGGCTCTGTGCGGCCCGGAGGAGGA | 1380 | |
| Qy | 1393 | CACAGACCCCGCTGCCGTGTGTGACGTGTCTGCCAGCACAGCAGCCCTGGCAGGTGA | 1452 | |
| Db | 1381 | CACAGACCCCGCTGCCGTGTGTGACGTGTCTGCCAGCACAGCAGCCCTGGCAGGTGA | 1440 | |
| Qy | 1453 | CGGTTCTGTCGGGGCTGCCGTGCCCGGGTGTGTGCCCCCAGGCGCTCTGGGGTCCAGGCA | 1512 | |
| Db | 1441 | CGGTTCTGTCGGGGCTGCCGTGCCCGGGTGTGTGCCCCCAGGCGCTCTGGGGTCCAGGCA | 1500 | |
| Qy | 1513 | CAACGAACCGCGTCTCTCAGGAACACCAAGAAGTTATCTCCCTGGGAGACGATGCCAA | 1572 | |
| Db | 1501 | CAACGAACCGCGTCTCTCAGGAACACCAAGAAGTTATCTCTCCCTGGGAGACGATGCCAA | 1560 | |
| Qy | 1573 | GCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGCTGCGGGACTGCGCTTGCGCTGCAG | 1632 | |
| Db | 1561 | GCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGCTGCGGGACTGCGCTTGCGCTGCAG | 1620 | |
| Qy | 1633 | GAGCCAGGGTTGGCTGTGTTCCGGCCGAGAGACCGCTCTGCGTAGGAGATCCTGGC | 1692 | |
| Db | 1621 | GAGCCAGGGTTGGCTGTGTTCCGGCCGAGAGACCGCTCTGCGTAGGAGATCCTGGC | 1680 | |
| Qy | 1693 | CAAGTTCTCTCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA | 1752 | |
| Db | 1681 | CAAGTTCTCTCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA | 1740 | |
| Qy | 1753 | TGTACGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTACCGAAAGTGTCTGGAG | 1812 | |
| Db | 1741 | TGTACGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTACCGAAAGTGTCTGGAG | 1800 | |
| Qy | 1813 | CAAGTTGCAAGCATTTGGAATCAGACGACCTTGAAGAGGTGTCAGCTGCGGAGCTGTC | 1872 | |
| Db | 1801 | CAAGTTGCAAGCATTTGGAATCAGACGACCTTGAAGAGGTGTCAGCTGCGGAGCTGTC | 1860 | |
| Qy | 1873 | GGAAAGCAGGTCAGCAGCATCGGAAGCCAGGCGCGCCCTGCTGAGCTCCAGACTCG | 1932 | |
| Db | 1861 | GGAAAGCAGGTCAGCAGCATCGGAAGCCAGGCGCGCCCTGCTGAGCTCCAGACTCG | 1920 | |
| Qy | 1933 | CTTTCATCCCAAGCCTGACGGCTGCGCGCGATTGTGAACATGGACTACGCTGCGGAGC | 1992 | |
| Db | 1921 | CTTTCATCCCAAGCCTGACGGCTGCGCGCGATTGTGAACATGGACTACGCTGCGGAGC | 1980 | |
| Qy | 1993 | CAGAACGTTCCGAGAGAAAGAGGCGCAGGCTCTACCTCGAGGGTGAAGGCACTGTT | 2052 | |
| Db | 1981 | CAGAACGTTCCGAGAGAAAGAGGCGCAGGCTCTACCTCGAGGGTGAAGGCACTGTT | 2040 | |
| Qy | 2053 | CAGCGTGCTCAACTACGAGGGGCGGCGCCCGCCCTCCCTGCTGCTGCTGCTGG | 2112 | |
| Db | 2041 | CAGCGTGCTCAACTACGAGGGGCGGCGCCCGCCCTCCCTGCTGCTGCTGCTGG | 2100 | |
| Qy | 2113 | CCTGGAGATATCCACAGGGCCTGGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTG | 2172 | |
| Db | 2101 | CCTGGAGATATCCACAGGGCCTGGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTG | 2160 | |
| Qy | 2173 | GCGCCCTGAGCTGATTTGTCAAGGTGATGTGAGGGGCGGTACGACACCATCCGCCA | 2232 | |
| Db | 2161 | GCGCCCTGAGCTGATTTGTCAAGGTGATGTGAGGGGCGGTACGACACCATCCGCCA | 2220 | |
| Qy | 2233 | GGACAGGCTCACGGAGGTATCGCCAGCATCATCAACCCAGACACGTAAGGCTGG | 2292 | |
| Db | 2221 | GGACAGGCTCACGGAGGTATCGCCAGCATCATCAACCCAGACACGTAAGGCTGG | 2280 | |
| Qy | 2293 | TCGGTATGCCGTGGTCCAGAGGCGCCCATGGGACGCTCCGCAAGGCTTCAAGAGCA | 2352 | |
| Db | 2281 | TCGGTATGCCGTGGTCCAGAGGCGCCCATGGGACGCTCCGCAAGGCTTCAAGAGCA | 2340 | |
| Qy | 2353 | CGTCTCTACCTTGACAGACCTCCAGCCGTACATGGACAGTTCTGGGCTCACTGCAGGA | 2412 | |

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Db 2401 GACCAGCCGCTGAGGGATGCGGTGCTCATCGAGCAGAGTCTCTCCCTGAATGAGCCAG 2460
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QY 2773 GACAGTGGTGAATTCCTCTGTAAGACGAGGCGCTGGGTGGCAGCGCTTTTGTTCAGAT 2832
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QY 3073 CAAATCTCTCTGCTGCAGCGTACAGGTTTACAGCATGTGCTGCAGCTCCCATTTCA 3132
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Db 3361 GCTGAGTCGAGACTCCCGGGGACGAGCTGACTGCTGAGGCGCGACCGCAACCCGCG 3420
QY 3433 ACTGCGCTCAGACTTCAAGACCATCTCTGACTGATGGCCACCGCCACAGCGCGCGA 3492
Db 3421 ACTGCGCTCAGACTTCAAGACCATCTCTGACTGATGGCCACCGCCACAGCGCGCGA 3480

RESULT 6

US-09-128-354-1
; Sequence 1, Application US/09128354
; Patent No. 6337200

; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants

; FILE REFERENCE: 015389-003310US

; CURRENT APPLICATION NUMBER: US/09/128,354

; EARLIER FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 08/851,843

; EARLIER FILING DATE: 1997-05-06

; EARLIER APPLICATION NUMBER: US 08/854,050

; EARLIER FILING DATE: 1997-05-09

; EARLIER APPLICATION NUMBER: US 08/911,312

; EARLIER FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: US 08/912,951

; EARLIER FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: US 08/915,503

; EARLIER FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: WO PCT/US97/17618

; EARLIER FILING DATE: 1997-10-01

; EARLIER APPLICATION NUMBER: WO PCT/US97/17885

; EARLIER FILING DATE: 1997-10-01

; EARLIER APPLICATION NUMBER: US 08/974,549

; EARLIER FILING DATE: 1997-11-19

; EARLIER APPLICATION NUMBER: US 08/974,584

; EARLIER FILING DATE: 1997-11-19

; EARLIER APPLICATION NUMBER: US 09/052,864

; EARLIER FILING DATE: 1998-03-31

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 4015

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (56)..(3454)

OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA

Query Match 99.6%; Score 3784.4; DB 4; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2161 GCCCGCTGAGCTGCTACTTTGTTGAAGGTGGATGTGACGGGGGCGGTACGACACCAATCCCCCA 2220
QY 2233 GGACAGGCTCACGAGGTGCTATCCGCCAGCATCATCAAAACCCAGAAACAGCTACTGCGTGGC 2292
Db 2221 GGACAGGCTCACGAGGTGCTATCCGCCAGCATCATCAAAACCCAGAAACAGCTACTGCGTGGC 2280
QY 2293 TCGGTATGCGGTGCTCCAGAGGCCGCCCATGAGGACAGTCCGGAAGGCCCTTCAAGAGCCA 2352
Db 2281 TCGGTATGCGGTGCTCCAGAGGCCGCCCATGAGGACAGTCCGGAAGGCCCTTCAAGAGCCA 2340
QY 2353 CGTCTCTACTCTTACAGAGCTCCAGCGGTACATGCGCAGAGTTCGTGGCTCACCTGACGGA 2412
Db 2341 CGTCTCTACTCTTACAGAGCTCCAGCGGTACATGCGCAGAGTTCGTGGCTCACCTGACGGA 2400
QY 2413 GACACGCCGCTGAGGATGCCCTGCTCATCGACAGAGCTCTCCCTGAATGAGGCCAG 2472
Db 2401 GACACGCCGCTGAGGATGCCCTGCTCATCGACAGAGTTCCTCCCTGAATGAGGCCAG 2460
QY 2473 CAGTGGCTCTTCCAGCGTCTTCTACGCTTATGTCGACACCGCGGTGGCATCAGGGG 2532
Db 2461 CAGTGGCTCTTCCAGCGTCTTCTACGCTTATGTCGACACCGCGGTGGCATCAGGGG 2520
QY 2533 CAACTGCTAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG 2592
Db 2521 CAACTGCTAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG 2580
QY 2593 CAGCCTGTGCTACGGCGACATGAGAAACAGCTGTTTGGGGGATTCGGCGGACGGGCT 2652
Db 2581 CAGCCTGTGCTACGGCGACATGAGAAACAGCTGTTTGGGGGATTCGGCGGACGGGCT 2640
QY 2653 GCTCCTGCGTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACCGGAAAC 2712
Db 2641 GCTCCTGCGTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACCGGAAAC 2700
QY 2713 CTTCCTCAGGACCTCGTCCGAGGTGCTCCTGAGTATGCTGCTGAGTGAACCTGCGGAA 2772
Db 2701 CTTCCTCAGGACCTCGTCCGAGGTGCTCCTGAGTATGCTGCTGAGTGAACCTGCGGAA 2760
QY 2773 GACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTTCAGAT 2832
Db 2761 GACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTTCAGAT 2820
QY 2833 GCGGGCCACGCGCTATTCCTCTGTTGCGGCTGCTGCTGGATACCGGACCGCTGGAGGT 2892
Db 2821 GCGGGCCACGCGCTATTCCTCTGTTGCGGCTGCTGCTGGATACCGGACCGCTGGAGGT 2880
QY 2893 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGAGTCTCACCTTCAACCG 2952
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGAGTCTCACCTTCAACCG 2940
QY 2953 CGGCTTCAAGGCTGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTCGGGCTGAAGTG 3012
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTCGGGCTGAAGTG 3000
QY 3013 TCACAGCCTGTTCTGTGATTTGCAGTGAACAGCTCCAGAGCGGTGTCACCAACATCTA 3072
Db 3001 TCACAGCCTGTTCTGTGATTTGCAGTGAACAGCTCCAGAGCGGTGTCACCAACATCTA 3060
QY 3073 CAAGATCTCTCTGCTGACGCGGTACAGGTTTACGCGATGTGCTCAGCTCCCATTTCA 3132
Db 3061 CAAGATCTCTCTGCTGACGCGGTACAGGTTTACGCGATGTGCTCAGCTCCCATTTCA 3120
QY 3133 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGGCCCTCCCT 3192
Db 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGGCCCTCCCT 3180
QY 3193 CTGCTACTCATCTGAAAGCCCAAGACCGAGGATGCTGCGGGGCCAAGGGCCCGC 3252
Db 3181 CTGCTACTCATCTGAAAGCCCAAGAACGAGGATGCTGCTGGGGGCCAAGGGCCCGC 3240
QY 3253 CGGCGCTCTGCCCTCGAGGCGGTGCAAGTGGCTGTCACCAAGCATTTCTGCTCAAGCT 3312
Db 3241 CGGCGCTCTGCCCTCGAGGCGGTGCAAGTGGCTGTCACCAAGCATTTCTGCTCAAGCT 3300

QY 3313 GACTCGACACCGCTGCTACCTTACCTTACCTGCGACCTCTCTGGGTCACTCAGGACAGCCAGAGCCA 3372
Db 3301 GACTCGACACCGCTGCTACCTTACCTTACCTGCGACCTCTCTGGGTCACTCAGGACAGCCAGAGCCA 3360
QY 3373 GCTGAGTTCGGAAGCTCCCGGGGACGAGCGCTGACTGCGCTTGAGGCGCGCAGCCAAACCGGC 3432
Db 3361 GCTGAGTTCGGAAGCTCCCGGGGACGAGCGCTGACTGCGCTTGAGGCGCGCAGCCAAACCGGC 3420
QY 3433 ACTGCGCTCAGACTTCAAGACCATCTTGGACTGATGGCCACCGCCACAGCCAGGCCGA 3492
Db 3421 ACTGCGCTCAGACTTCAAGACCATCTTGGACTGATGGCCACCGCCACAGCCAGGCCGA 3480
QY 3493 GACGACACACACGACGACCGCTGTCAGCGCGGCTTACGTCCAGGAGGAGGGGGCGGC 3552
Db 3481 GACGACACACACGACGACCGCTGTCAGCGCGGCTTACGTCCAGGAGGAGGGGGCGGC 3540
QY 3553 CACACCGAGCCCGCAGCGCTGAGGAGTCTGAGGCGCTGAGTGTGTTGGCCAGAGCGCTG 3612
Db 3541 CACACCGAGCCCGCAGCGCTGAGGAGTCTGAGGCGCTGAGTGTGTTGGCCAGAGCGCTG 3600
QY 3613 CATGTCGCGCTGAAGCTGAGTGTCCGGCTGAGGAGTCTGAGGCGCTGAGGAGTCTGAGGCGCTG 3672
Db 3601 CATGTCGCGCTGAAGCTGAGTGTCCGGCTGAGGAGTCTGAGGCGCTGAGGAGTCTGAGGCGCTG 3660
QY 3673 GAGTGTCCAGCACACCTGCGCTTTCACCTTCCCGCACAGCGCTGGCGCTCCAGCCCA 3732
Db 3661 GAGTGTCCAGCACACCTGCGCTTTCACCTTCCCGCACAGCGCTGGCGCTCCAGCCCA 3720
QY 3733 GGCGCAGCTTTCTCCAGAGGAGCGCGCTTCCACTTCCCGCACATAGGAATAGTCCATCC 3792
Db 3721 GGCGCAGCTTTCTCCAGAGGAGCGCGCTTCCACTTCCCGCACATAGGAATAGTCCATCC 3780
QY 3793 CCGTAT 3798
Db 3781 CCAGAT 3786

RESULT 7

US-09-675-321-1
; Sequence 1, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-09-675-321-1

Query Match 99.6%; Score 3784.4; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 GCAGCGCTGGTCTGCTGCGCAGCTGGGAGCCCTGGCCCGCCACCGCCCGGATGCC 72
Db 1 GCAGCGCTGGTCTGCTGCGCAGCTGGGAGCCCTGGCCCGCCACCGCCCGGATGCC 60

[illegible]

Db 2221 GACAGGCTCAGGAGGTCTACCCAGCATCATCAAAACCCAGAACACGTACTGCGTGGC 2280
QY TCGGTATGCGGTGTCAGAAAGCCGCGCATATGGGACAGCTCCGAAAGGCCCTTCAAGAGCCA 2352
Db TCGGTATGCGGTGTCAGAAAGCCGCGCATATGGGACAGCTCCGAAAGGCCCTTCAAGAGCCA 2340
QY CGTCTCTACCTTACAGACACTCAGCGGTATCATGCGACAGTTCGTGGCTCACCTGCAGGA 2412
Db CGTCTCTACCTTACAGACACTCAGCGGTATCATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
QY GACAGCCGCTCAGGAGTCCGCTGCTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG 2472
Db GACAGCCGCTCAGGAGTCCGCTGCTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460
QY CAGTGGCTCTTCGAGCTCTTCTACGCTTTCATGTGCCACACGCGGTGGCATCAGGGG 2532
Db CAGTGGCTCTTCGAGCTCTTCTACGCTTTCATGTGCCACACGCGGTGGCATCAGGGG 2520
QY CAAGTCTAGTCCAGTCCAGGGGATCCGCGAGGGGTCCATCTTCCACGCTGCTCTG 2592
Db CAAGTCTAGTCCAGTCCAGGGGATCCGCGAGGGGTCCATCTTCCACGCTGCTCTG 2580
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Db CAGCTGTGCTACGCGACATGAGAACAGCTGTTTGGGGGATTCGGCGGACGCGGCT 2640
QY GCTCTGCGCTTGTGTGATGATTTCTTGTGTGACACCTCACCTCACCCACCGGAAAC 2712
Db GCTCTGCGCTTGTGTGATGATTTCTTGTGTGACACCTCACCTCACCCACCGGAAAC 2700
QY CTCTCTCAGACCCCTGGTCGAGGTGTCCTGAGTATGGCTGCGGTGAACCTTGGGAA 2772
Db CTCTCTCAGACCCCTGGTCGAGGTGTCCTGAGTATGGCTGCGGTGAACCTTGGGAA 2760
QY GACAGTGTGAACTTCCCTGTAGAACGAGGCGCTGGGTGGACGCGCTTTTCTTCAGT 2832
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Db GCGCGCCAGCGGCTATTCCCTGTGCGGCGCTGCTGCTGATACCCGACCCCTGGAGGT 2880
QY GCAGAGGACTACTCAGTATGCGCGGACCTCCATCAGAGCAGTCTCACCTTCAACCG 2952
Db GCAGAGGACTACTCAGTATGCGCGGACCTCCATCAGAGCAGTCTCACCTTCAACCG 2940
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Db CGGCTTCAAGGCTGGAGGAACATGCTGCGAACTCTTTGGGCTCTGCGGCTGAAGTG 3000
QY TCACAGCCTGTTTCTGGATTTGAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3072
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QY CAAGATCTCTGCTCGAGCGGTACAGGTTTACGCGATGTGTGCTGAGTCCCATTTCA 3132
Db CAAGATCTCTGCTCGAGCGGTACAGGTTTACGCGATGTGTGCTGAGTCCCATTTCA 3120
QY TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGCGCTTCCCT 3192
Db TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGCGCTTCCCT 3180
QY CTGCTACTCTCTCTGAAAGCCAAAGAACAGGAGTGTGCTGGGGCCAAAGGCGCGC 3252
Db CTGCTACTCTCTCTGAAAGCCAAAGAACAGGAGTGTGCTGGGGCCAAAGGCGCGC 3240
QY CGGCGCTCTGCGCTCGAGGCGGTGAGTGGTGTGCCACCAAGCAATTCCTGCTCAAGCT 3312
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QY GACTCGACCGGTGCTCACCTACGTGCTGCTCTGCGGCTCACCTCAGACAGCCGACAGCA 3372
Db GACTCGACCGGTGCTCACCTACGTGCTGCTCTGCGGCTCACCTCAGACAGCCGACAGCA 3360

Db 3301 GACTCGACACCGGTGCTACCTACGTGCGACACTCTCTGGGGTCTACTCAGSACAGCCCAAGCGCA 3360
QY GCTGAGTCGGAAGTCCCGGGGACGAGCGCTGACTGCGCTGGAGGCCGACCAACCGGC 3432
Db GCTGAGTCGGAAGTCCCGGGGACGAGCGCTGACTGCGCTGGAGGCCGACCAACCGGC 3420
QY ACTGCCCTCAGACTTCAAGACCATCTCTGAGTGTGATGGCCACCGCCACAGCCAGGCCG 3492
Db ACTGCCCTCAGACTTCAAGACCATCTCTGAGTGTGATGGCCACCGCCACAGCCAGGCCG 3480
QY GAGCAGACACACGAGCCCTGTGTCAGCCGCGGCTCTAGTCCAGGGAGGAGGGCGGCC 3552
Db GAGCAGACACACGAGCCCTGTGTCAGCCGCGGCTCTAGTCCAGGGAGGAGGGCGGCC 3540
QY CACACCCAGCCGCGACCGCTGGAGTCTGAGGCGCTGAGTGTGCTGGCCGAGGCGCTG 3612
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QY GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCGACAGGCTGGCGCTCCAGCCCA 3732
Db GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCGACAGGCTGGCGCTCCAGCCCA 3720
QY GGCCAGCTTTTCTCACCAGAGCCGCGCTTCCACTCCCGACATAGGAATAGTCCATCC 3792
Db GGCCAGCTTTTCTCACCAGAGCCGCGCTTCCACTCCCGACATAGGAATAGTCCATCC 3780
QY CCTGAT 3798
Db CCAGAT 3786

RESULT 8

US-09-052-919-1

; Sequence 1, Application US/09052919

; Patent No. 644650

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Antisense Compositions for Detecting and

; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/052,919

; FILING DATE: 31-MAR-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

| Query Match | 99.6%; | Score 3784.4; | DB 4; | Length 4015; |
|-----------------------|-----------------|---|-----------|--------------|
| Best Local Similarity | 100.0%; | Prod. No. 0; | | |
| Matches 3785; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| QY | 13 | GCACGCGTGGTCTGCTGTGGCACAGTGGGAAGCCCTGGCCCGCGCCACCCCGCGATGCC | 72 | |
| Db | 1 | GCACGCGTGGTCTGCTGTGGCGACGTGGGAAGCCCTGGCCCGCGCCACCCCGCGATGCC | 60 | |
| QY | 73 | GCAGCGTCGCCGCTGCCAGCCGTGCCTCCTCTGCGCAGCCACATACCGCGAGGTGCT | 132 | |
| Db | 61 | CGCGGCTCCCGCTGCCAGCCGTGCCTCCTCTGCGCAGCCACATACCGCGAGGTGCT | 120 | |
| QY | 133 | CGCGCTGGCCACGTTCTTGGGGGGCCCTGGGGGGCCCGAGGGCTGGCGGCTGTGTGCACGCGG | 192 | |
| Db | 121 | CGCGCTGGCCACGTTCTTGGGGGGCCCTGGGGGGCCCGAGGGCTGGCGGCTGTGTGCACGCGG | 180 | |
| QY | 193 | GGACCCGGCGGGCTTTCCGGCGGCTGTGGGCCCAAGTCGCTGGTGCGCTGCCCTGGGAGCG | 252 | |
| Db | 181 | GGACCCGGCGGGCTTTCCGGCGGCTGTGTGGGCCCAAGTCGCTGGTGCGCTGCCCTGGGAGCG | 240 | |
| QY | 253 | ACGGCGCGCGCGCGCGCGCGCGCTCTTCGCCAGGTGTCTCTGCTGAAGAGAGTGGTGCG | 312 | |
| Db | 241 | ACGGCGCGCGCGCGCGCGCGCGCTCTTCGCCAGGTGTCTCTGCTGAAGAGAGTGGTGCG | 300 | |

| | | | |
|----|------|--|------|
| QY | 1393 | CACAGACCCCGTCGCTGGTGCAGCTGCTCCGCCACACAGACAGCCCTTGGCAGGTGA | 1451 |
| DB | 1381 | CACAGACCCCGTCGCTGGTGCAGCTGCTCCGCCACACAGACAGCCCTTGGCAGGTGA | 1440 |
| QY | 1453 | CGGCTTCGTGGGGCCCTCGCTGGCCCGGCTGTCGCCCCAGGCTCTGGGGCTCCAGGCA | 1512 |
| DB | 1441 | CGGCTTCGTGGGGCCCTCGCTGGCCCGGCTGTCGCCCCAGGCTCTGGGGCTCCAGGCA | 1500 |
| QY | 1513 | CAACGAACCGCCCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGGAAGCATGCCAA | 1572 |
| DB | 1501 | CAACGAACCGCCCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGGAAGCATGCCAA | 1560 |
| QY | 1573 | GCTCTCGCTGCAGGAGTGACGTGGAAAGATGAGCGTGGGAGTGCCTTGGCTGGCGCAG | 1632 |
| DB | 1561 | GCTCTCGCTGCAGGAGTGACGTGGAAAGATGAGCGTGGGAGTGCCTTGGCTGGCGCAG | 1620 |
| QY | 1633 | GAGCCCAAGGGTGGCTGCTTCCGGCCGCAGAGCACCCGTCTGCGTGAGAGATCTCTGGC | 1692 |
| DB | 1621 | GAGCCCAAGGGTGGCTGCTTCCGGCCGCAGAGCACCCGTCTGCGTGAGAGATCTCTGGC | 1680 |
| QY | 1693 | CAAGTTCTCTGCACCTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGTCTTTCTTTTAA | 1752 |
| DB | 1681 | CAAGTTCTCTGCACCTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGTCTTTCTTTTAA | 1740 |
| QY | 1753 | TGTCACGGAGACACAGTTTCAAAGAACAGGCTCTTTTTCCTACCGGAAGAGTGTCTGGAG | 1812 |
| DB | 1741 | TGTCACGGAGACACAGTTTCAAAGAACAGGCTCTTTTTCCTACCGGAAGAGTGTCTGGAG | 1800 |
| QY | 1813 | CAAGTGTCAAAGCATTCGAATCAGACAGCACTGTGAAGAGGTGCACGTGGGAGCTGTC | 1872 |
| DB | 1801 | CAAGTGTCAAAGCATTCGAATCAGACAGCACTGTGAAGAGGTGCACGTGGGAGCTGTC | 1860 |
| QY | 1873 | GGAAGCAGAGGTTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTCAGCTCCAGACTCCG | 1932 |
| DB | 1861 | GGAAGCAGAGGTTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTCAGCTCCAGACTCCG | 1920 |
| QY | 1933 | CTTCATCCCAAGCCTGACGGCTGCGGGCGATTGTGAACATGACTACCTGTGTGGGAGC | 1992 |
| DB | 1921 | CTTCATCCCAAGCCTGACGGCTGCGGGCGATTGTGAACATGACTACCTGTGTGGGAGC | 1980 |
| QY | 1993 | CAGAACTTCGCGACAGAAAGAGGGCCGAGCGTCTACCTCCGAGGTGAAGCACTGTT | 2052 |
| DB | 1981 | CAGAACTTCGCGACAGAAAGAGGGCCGAGCGTCTACCTCCGAGGTGAAGCACTGTT | 2040 |
| QY | 2053 | CAGCGTCTCAACTACGAGCGGGCGCGCGCCCGCCCTCCTGGGGCCCTCTGTGTGGG | 2112 |
| DB | 2041 | CAGCGTCTCAACTACGAGCGGGCGCGCGCCCGCCCTCCTGTGTGGG | 2100 |
| QY | 2113 | CCTGGAGCATATCCACAGGCGCTGGCGCACCTTCGTGCTCGTGGGGCCCGAGACCC | 2172 |
| DB | 2101 | CCTGGAGCATATCCACAGGCGCTGGCGCACCTTCGTGCTCGTGGGGCCCGAGACCC | 2160 |
| QY | 2173 | GCGCCCTGAGCTGACTTTCGAAAGTGGATGTGAGGGGCGCTACGACACCACTCCCCCA | 2232 |
| DB | 2161 | GCGCCCTGAGCTGACTTTCGAAAGTGGATGTGAGGGGCGCTACGACACCACTCCCCCA | 2220 |
| QY | 2233 | GGACAGGCTCACGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACACGTCTGCGTGGC | 2292 |
| DB | 2221 | GGACAGGCTCACGGAGGTCTATCGCCAGCATCATCAAAACCCAGAACACGTCTGCGTGGC | 2280 |
| QY | 2293 | TCGATATCCCGTGTCCAGAGGCCGCCCATGGSCAGCTCCCGAAGSCCTTCAAGAGCCA | 2352 |
| DB | 2281 | TCGATATCCCGTGTCCAGAGGCCGCCCATGGSCAGCTCCCGAAGSCCTTCAAGAGCCA | 2340 |
| QY | 2353 | CGTCTCTACCTTGACACACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGAGGA | 2412 |
| DB | 2341 | CGTCTCTACCTTGACACACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGAGGA | 2400 |
| QY | 2413 | GACCAGCCCGCTGAGGATCCGCTCGCTCATCAGACAGAGCTCTCTCCCTGAATCAGGCCAG | 2472 |
| DB | 2401 | GACCAGCCCGCTGAGGATCCGCTCGCTCATCAGACAGAGCTCTCTCCCTGAATCAGGCCAG | 2460 |
| QY | 2473 | CAGTGGCCTCTTCGACGCTCTTCTCTACGCTTCATGTGCCACACGACGCGCTGCATCAGGG | 2532 |

| | | | |
|----|------|--|------|
| Db | 2461 | CAAGTGGCCCTTTCGAGCTCTTCTACGCTTCATGTCGCCACACCGCGTGCGCATCAGGG | 2520 |
| QY | 2533 | CAAGTCTTACGTCACGTCAGCGAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG | 2592 |
| Db | 2521 | CAAGTCTTACGTCACGTCAGCGAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG | 2580 |
| QY | 2593 | CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCCGCGGACAGGGCT | 2652 |
| Db | 2581 | CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCCGCGGACAGGGCT | 2640 |
| QY | 2653 | GCTCCTGGCTTGGTGGATGATTTCTTGTGTGGTGCACCTCACCCTACCCACGCGAAAC | 2712 |
| Db | 2641 | GCTCCTGGCTTGGTGGATGATTTCTTGTGTGGTGCACCTCACCCTACCCACGCGAAAC | 2700 |
| QY | 2713 | CTTTCCTCAGSACCCTGGTCCGAGGTGTCCTCGAGTATGCTGCGTGAGTCAACTTCGGGA | 2772 |
| Db | 2701 | CTTTCCTCAGSACCCTGGTCCGAGGTGTCCTCGAGTATGCTGCGTGAGTCAACTTCGGGA | 2760 |
| QY | 2773 | GACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTTCAGAT | 2832 |
| Db | 2761 | GACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTTCAGAT | 2820 |
| QY | 2833 | GCGGGCCACGGGCTATTCCCTGTGTGGGCTGCTGCTGGATACCCGAGCCCTGGAGGT | 2892 |
| Db | 2821 | GCGGGCCACGGGCTATTCCCTGTGTGGGCTGCTGCTGGATACCCGAGCCCTGGAGGT | 2880 |
| QY | 2893 | GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCCTCAACCG | 2952 |
| Db | 2881 | GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCCTCAACCG | 2940 |
| QY | 2953 | CGGCTTCAAGGCTGGGAGAACATGCTGCGCAAACCTTTTGGGGCTTCGGGCTGAAGTG | 3012 |
| Db | 2941 | CGGCTTCAAGGCTGGGAGAACATGCTGCGCAAACCTTTTGGGGCTTCGGGCTGAAGTG | 3000 |
| QY | 3013 | TCACAGGCTGTTCTCGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA | 3072 |
| Db | 3001 | TCACAGGCTGTTCTCGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA | 3060 |
| QY | 3073 | CAAGATCTCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTTCA | 3132 |
| Db | 3061 | CAAGATCTCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTTCA | 3120 |
| QY | 3133 | TCAGCAAGTTTGAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGCGCTCCCT | 3192 |
| Db | 3121 | TCAGCAAGTTTGAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGCGCTCCCT | 3180 |
| QY | 3193 | CTGCTACTCGATCCTGAAGCCAAAGACAGGGATGTGCTGCGGGGCCAAGGGCGCCGC | 3252 |
| Db | 3181 | CTGCTACTCGATCCTGAAGCCAAAGACAGGGATGTGCTGCGGGGCCAAGGGCGCCGC | 3240 |
| QY | 3253 | CGGCGCTCTGCCCTCCGAGGCGTGCAGTGGCTGTGCCACCAAGCAATTCCTGCTCAAGCT | 3312 |
| Db | 3241 | CGGCGCTCTGCCCTCCGAGGCGTGCAGTGGCTGTGCCACCAAGCAATTCCTGCTCAAGCT | 3300 |
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| Db | 3421 | ACTGCCCTCAGACTTCAAGACCAATCTTGGACTGATGGCCACCGCCCAACGAGGCCGA | 3480 |
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RESULT 9

US-08-912-951-1
Sequence 1, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912.951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-00260005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
OTHER INFORMATION: /note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
US-08-912-951-1

Query Match 99.6%; Score 3784.4; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 GCAGCGCTGCGTCTGCTGCGCACGCTGGGAAGCCCTGGCCGCGCCACCCCGCGATGCC 72
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RESULT 10
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; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527

; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3

Query Match 99.6%; Score 3784.4; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
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| | | | | | | |
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| QY | 913 | CACCTCTTTTGGAGGTGGCCTCTCTGGCAGCGGCCACTCCACCCATCCGTGGGCGCCA | 972 | 1993 | CAGAGGTTCCGACAGAAAAGAGGCGCAGCGTCTCACTCGAGGGTGAAGCACTGTT | 2052 |
| Db | 901 | CACCTCTTTTGGAGGTGGCCTCTCTGGCAGCGGCCACTCCACCCATCCGTGGGCGCCA | 960 | 1981 | CAGAGGTTCCGACAGAAAAGAGGCGCAGCGTCTCACTCGAGGGTGAAGCACTGTT | 2040 |
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| QY | 1213 | GCCCCAGCGCTACTGCAAAATGGGCCCTTCTTCTGGAGCTGCTTGGGAACACGCGCA | 1272 | 2293 | TGGGTATGCCGTGGTCCAGAAAGGCCGCCCATGGGCAGCTCCGCAAGGCCTTCAAGAGCCA | 2352 |
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| QY | 1333 | AGCCGCTGTCTGTGCCGGGAGAACCCAGGCTCTGTGGGGCCCCCGAGGAGGGA | 1392 | 2413 | GACCAAGCCGCTGAGGGATGCCGTCTCATCGACGAGAGCTCCTCCTGAATGAGGCCAG | 2472 |
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| Db | 1381 | CACAGACCCGCTGCGCTGGTGAGTGTCTCCGACAGACAGAGCCCTGGCAGGTGA | 1440 | 2461 | CAGTGGCCTCTTCGAGCGTCTTCCCTAGCGTCTATGTGCCACACGCGCGTGGGCAACAGGG | 2520 |
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| QY | 1813 | CAAGTTGCAAGCATTTGGAATCAGACAGCACATTTGAAGAGGTGCCAGCTGCGGAGCTGTC | 1872 | 2893 | GCAGACGACTACTCCAGCTATGCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG | 2952 |
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[illegible]

RESULT 11
US-08-974-549A-343 ✓
; Sequence 343, Application US/08974549A
; Patent No. 6166178

; PATENT NO. 6166178
: GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B

APPLICANT: MORIN, Gregg B.

APPLICANT: Harley, Calvin B

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00261005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of
US-08-974-549A-343"

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|-----------------------|-------|--------------|------|-------------|
| Query Match | 99.5% | Score 3779.2 | DB 3 | Length 4037 |
| Best Local Similarity | 99.9% | Pred. No. 0 | | |

QY 13 GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGATGCC 72

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1 GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGATGCC 60

QY 73 GCGCGTCCCGCTGCGAGCCGTCCTGCTGCGCAGCCACTACCGGAGGTGCT 132

Db 61 GCGCGCTCCCGCTCCGAGCGGTGGCTCCCTGCTGGGAGCCACTACGGGAGGTGCT 120
QY 133 GCGCGTGGCCACGTTCTGCGGCGCTTGGGGCCCCAGGGCTGCGGCTGCTGTCAGGCGCG 192
Db 121 GCGCGTGGCCACGTTCTGCGGCGCTTGGGGCCCCAGGGCTGCGGCTGCTGTCAGGCGCG 180
QY 193 GGACCGGGGGCTTTCGGGGCGTGGTGGCCCAAGTCCCTGGTGGTGGTGGTGGTGGTGGTGG 252
Db 181 GGACCGGGGGCTTTCGGGGCGTGGTGGCCCAAGTCCCTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 253 ACGGCCCGCCCGCCCGCCCTTCTCCGCAAGTGTCTGCTCAAGGAGCTGTGTGG 312
Db 241 ACGGCCCGCCCGCCCGCCCTTCTCCGCAAGTGTCTGCTCAAGGAGCTGTGTGG 300
QY 313 CCGAGTGTCTGCAAGAGCTGTGGAGCGCGGCGCGAAGACGTGCTGGCCCTCGGCTTCGC 372
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QY 373 GCTGCTGGACGGGGCCCCGGGGCCCCCGGAGGCGCTTCAACCACGAGCTGGCGAGCTA 432
Db 361 GCTGCTGGACGGGGCCCCGGGGCCCCCGGAGGCGCTTCAACCACGAGCTGGCGAGCTA 420
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QY 493 CCGCGTGGGCGACGAGTGTCTGGTTCACTGTGTGCACTGCGGCGCTCTTTGTGTGT 552
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QY 613 TCAGGCGCGCGCCCGCCACAGCTAGTGGACCCCGAAGCGCTGGGATGCAAGCGGC 672
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DB 3481 GAGCAGACACAGAGCCCTGTCAGCGCGGCTCTACGTCCTCCAGGAGGAGGGCGGCGC 3540
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RESULT 12
US-08-851-843A-173
Sequence 173, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4029 base pairs
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;   TOPOLOGY: linear
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; OTHER INFORMATION: human TR1 cDNA insert of
; OTHER INFORMATION: plasmid pGRN121"
; US-08-851-843A-173

Query Match          95.3%; Score 3618.6; DB 3; Length 4029;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;

QY 13 GCAGCGCTCGCTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCCCGCGGATGCC 72
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Db 1 GCAGCGCTGGCTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCCCGCGGATGCC 60

QY 73 GCGCGTCCCGGTGCGGAGCGGTGGCTCCCTGTGTCGACGACCTACCGGAGTGCT 132
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Db 61 GCGCGTCCCGGTGCGGAGCGGTGGCTCCCTGTGTCGACGACCTACCGGAGTGCT 120

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Db 1075 NCCTCTCTTCTACTCAATATATCTAGGCGCCAGCTGACTGCGGTTCGGAGGTTCTGTG 1134
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```


APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610DS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for
human TRT cDNA insert of
OTHER INFORMATION: plasmid pGRN121"
us-08-974-549A-292

| Query Match | 95.3% | Score 3618.6; | DB 3; | Length 4029; | |
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| Best Local Similarity | 98.3%; | Pred. No. 0; | | | |
| Matches 3725; | Conservative | 0; | Mismatches 54; | Indels 9; | Gaps 8; |
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| Qy | 73 | CGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGAGCCACCTACCGGAGGTGCT | 132 | | |
| Db | 61 | CGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGAGCCACCTACCGGAGGTGCT | 120 | | |
| Qy | 133 | GCGCTGGCCACAGTTGCTGCGCGCCCTGGGGCCCGCAGGGCTGGCGGTGCTGCGAGCGGG | 192 | | |
| Db | 121 | GCGCTGGCCACAGTTGCTGCGCGCCCTGGGGCCCGCAGGGCTGGCGGTGCTGCGAGCGGG | 180 | | |
| Qy | 193 | GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGGCTGGTGGCTGGCCCTGGGACGC | 252 | | |
| Db | 181 | GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGGCTGGTGGCTGGCCCTGGGANGN | 240 | | |
| Qy | 253 | ACGGCCCGCCCGCCCGCCCTCTTCCGCGCAGGTGCTGGTGGCCAGTGGCTGGCTGGGACGC | 312 | | |
| Db | 241 | ANGCNGCCCGCCCGCCCTCTTCCGCGCAGGTGCTGGTGGCTGGTGGCTGGCCCTGGGANGN | 300 | | |
| Qy | 313 | CCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGCTGGCTTTCGGCTTTCGC | 372 | | |
| Db | 301 | CCGAGTGTGTCANANGTGTGCGANCGCGCGCGAAGACGTGCTGGCTTTCGGCTTTCGC | 360 | | |
| Qy | 373 | GCTGCTGGACGGGCGCGCGGGGCGCCCGCGAGGCGCTTACACACAGCGCTGCGCAGCTA | 432 | | |
| Db | 361 | GCTGCTGGACGGGCGCGCGGGGCGCCCGCGAGGCGCTTACACACAGCGCTGCGCAGCTA | 420 | | |
| Qy | 433 | CTGCGCCCAACACAGGTGACCGACGACTGCGGGGGAGCGGGCGTGGGGGTGCTGCTGCG | 492 | | |
| Db | 421 | CCTGCCCAACACAGGTGACCGACGACTGCGGGGGAGCGGGCGTGGGGGTGCTGCTGCG | 480 | | |
| Qy | 493 | CCGCTGGGCGACGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 552 | | |
| Db | 481 | CCGCTGGGCGACGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 540 | | |
| Qy | 553 | GGCTCCAGCTGCGCCTACCAAGTGTGCGGGGCGCGCTGTACACAGCTGCGCGCTGCGAC | 612 | | |
| Db | 541 | GGNTCCAGCTGCGCCTACCAAGTGTGCGGGGCGCGCTGTACACAGCTGCGCGCTGCGAC | 600 | | |
| Qy | 613 | TCAGGGCG | 672 | | |
| Db | 601 | TCAGGGCG | 658 | | |
| Qy | 673 | CTGGAACCATAGCTGAGGGAGCGGGGTCCCGCTGGGCTGCGACGCCCGGGTGGGAG | 732 | | |
| Db | 659 | CTGGAACCATAGCTGAGGGAGCGGGGTCCCGCTGGGCTGCGACGCCCGGGTGGGAG | 717 | | |
| Qy | 733 | GAGCGCGGGGCGAGTCCAGCGCGAAGTGTGCGGTTCGCCAAGAGGCGCGCGCGCGCGCG | 792 | | |
| Db | 718 | GAGCGCGGGGCGAGTCCAGCGCGAAGTGTGCGGTTCGCCAAGAGGCGCGCGCGCGCGCG | 777 | | |
| Qy | 793 | TGCCCCCTGACCGGAGCG | 852 | | |
| Db | 778 | TGCCCCCTGACCGGAGCG | 837 | | |
| Qy | 853 | CGCTGGACCGAGTGACCGGTGCTTCTGTGTGGTGTACCTGCCAGACGCCCGCGAAGAC | 912 | | |
| Db | 838 | GCCTGGACCGAGTGACCGGTGCTTCTGTGTGGTGTACCTGCCAGACGCCCGCGAAGAC | 897 | | |
| Qy | 913 | CACCTCTTTGGAGGGTGCCTCTCTGTGCGACGCGCGCACTCCACCCATCTCGTGGCGCGCA | 972 | | |
| Db | 898 | CACCTCTTTGGAGGGTGCCTCTCTGTGCGACGCGCGCACTCCACCCATCTCGTGGCGCGCA | 957 | | |
| Qy | 973 | GCACCG | 1032 | | |
| Db | 958 | GCACCG | 1016 | | |

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|----|------|---|------|
| Qy | 1033 | CCCGGTGTACGCCGAGACCAAGCACTTTCCTCTACTCTCTACGGCGACAAGGAGCAGTGGC | 1099 |
| Db | 1017 | CCCGGTGTACGCCGAGACCAAGCACTTTCCTCTACTCTCTACGGCGACAAGNA--CACTGGC | 1074 |
| Qy | 1093 | GCCCTCCTTCTACTC-AGCTCTGTAGGCCCAAGCCTGACTGGCGTTCGGAGCTCGTGG | 1151 |
| Db | 1075 | NCCCTCCTTCTACTCAATATATCTGAGGCCAGCCTGACTGGCGTTCGGAGGTTTCGTG | 1134 |
| Qy | 1152 | AGACCATCTTTCTGGGTTCACAGCCCTTGGATGCCAGGGACTCCCCGACAGTTTGC | 1211 |
| Db | 1135 | GAGACANTCTTTCTGGTTCACAGCCTTGGATGCCA-GGATTCCCGCAGGTTGCCCGCC | 1193 |
| Qy | 1212 | TGCCCCAGCGCTACTTGGCAATATGGGCCCTCTGTTTCTGTGAGCTGTCTGGGAACACAGCGC | 1271 |
| Db | 1194 | TGCCCCAGCGNTACTTGGCAATATGGGCCCTCTGTTTCTGTGAGCTGTCTGGGAACACAGCGC | 1253 |
| Qy | 1272 | AGTGCCCTACGGGGTCTCTCAAGACGCACATGCCGCTGCCAGCTGCGGTCAACCCAG | 1331 |
| Db | 1254 | AGTGCCCTACGGGGTGTTCCTCAAGACGCACATGCCGCTGCCAGCTGCGGTCAACCCAG | 1311 |
| Qy | 1332 | CAGCCGGTGTCTTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGG | 1391 |
| Db | 1314 | CAGCCGGTGTCTTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGG | 1373 |
| Qy | 1392 | -ACACAGACCCCGTGGCGTGTGTGACGTCTCTCGCGACACAGCAGCCCTGGCAGGTG | 1450 |
| Db | 1374 | AACACAGACCCCGTGGCGTGTGTGACGTCTCTCGCGACACAGCAGCCCTGGCAGGTG | 1433 |
| Qy | 1451 | TAGGGCTTCGTGGGGCTGCCTGCGCGCGCTGGTGCCTTCTCCCTGGGGAAGCATGCC | 1510 |
| Db | 1434 | TAGGGCTTCGTGGGGCTGCCTGCGCGCGCTGGTGCCTTCTCCCTGGGAGCATGCC | 1493 |
| Qy | 1511 | CACAAGAACCGCGCTTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCC | 1570 |
| Db | 1494 | CACAAGAACCGCGCTTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCC | 1553 |
| Qy | 1571 | AACTCTCGTGCAGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGC | 1630 |
| Db | 1554 | AACTCTCGTGCAGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCGC | 1613 |
| Qy | 1631 | AGGAGCCAGGGGTGTGCTGTGTTCGGCGCGACGACCGTCTGAGTGGAGAGATCCCTG | 1690 |
| Db | 1614 | AGGAGCCAGGGGTGTGCTGTGTTCGGCGCGACGACCGTCTGAGTGGAGAGATCCCTG | 1673 |
| Qy | 1691 | GCCAACTTCCTGCACCTGGCTGATGAGTGTGACGTGCTGAGTGTCTCAAGTCTTCTTT | 1750 |
| Db | 1674 | GCCAACTTCCTGCACCTGGCTGATGAGTGTGACGTGCTGAGTGTCTCAAGTCTTCTTT | 1733 |
| Qy | 1751 | TATGTACGGAGACACAGTTTCAAAGACAGAGCTCTTTTTCACCGGAAGAGTGTCTG | 1810 |
| Db | 1734 | TATGTACGGAGACACAGTTTCAAAGACAGAGCTCTTTTTCACCGGAAGAGTGTCTG | 1793 |
| Qy | 1811 | AGCAAGTTGCAAGCATTGAANTCAGACAGCACTTGAAGGGTGTGAGTGGGAGCTCTG | 1870 |
| Db | 1794 | AGCAAGTTGCAAGCATTGAANTCAGACAGCACTTGAAGGGTGTGAGTGGGAGCTCTG | 1853 |
| Qy | 1871 | TCGGAAGCAGAGTTCAGGAGCATTCGGGAAGCCAGGCCCTGCTGAGCTCCAGACTC | 1930 |
| Db | 1854 | TCGGAAGCAGAGTTCAGGAGCATTCGGGAAGCCAGGCCCTGCTGAGCTCCAGACTC | 1913 |
| Qy | 1931 | CGTTTATCCCCAAGCCTTGACGGGCTGCGGCGGATGTTGAACATGAGTACGTCTGTGGGA | 1990 |
| Db | 1914 | CGTTTATCCCCAAGCCTTGACGGGCTGCGGCGGATGTTGAACATGAGTACGTCTGTGGGA | 1973 |
| Qy | 1991 | GCCAGAACGTTCCGAGAGAAAGAGGCCGAGCGTCTCACCTCGAGGTTGAGGCGACTG | 2050 |
| Db | 1974 | GCCAGAACGTTCCGAGAGAAAGAGGCCGAGCGTCTCACCTCGAGGTTGAGGCGACTG | 2033 |
| Qy | 2051 | TTCAGCGTGTCTAACTACGAGCGGGCGCGGCCCGCGCTCTCTGGCGCCTCTGTGTCTG | 2110 |
| Db | 2034 | TTCAGCGTGTCTAACTACGAGCGGGCGCGGCCCGCGCTCTCTGGCGCCTCTGTGTCTG | 2093 |
| Qy | 2111 | GGCCTGGAGATATCCACAGGGCCTGGCGCACTTCTGTGTCTGTGGGGGCCACAGGAC | 2170 |

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| 2094 | Db | GGCTGGACGATATCCACAGGGCTGGGCGCACCTTCGTGCTGCGTGTGCGGCGCCAGGAC | 2153 |
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| 2154 | Db | CCGCGCGCTGAGCTGTACTTTGTTCAGAGTGGATGTGACGGGCGCGTACGACACCATCCCC | 2213 |
| 2231 | Qy | CAGGACAGGCTCACGGAGGTTCATCGGCAGCATCATCAAAACCCAGAAACACGTACTGCGTG | 2290 |
| 2214 | Db | CAGGACAGGCTACGGAGGTTCATCGGCAGCATCATCAAAACCCAGAAACACGTACTGCGTG | 2273 |
| 2291 | Qy | CGTCGGTATGCCGTGTGTCAGAAAGCGCGCCATGGGCACGTCCGCAAGGCCCTCAAGAGC | 2350 |
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| 2411 | Qy | GAGACAGCCCGCTGAGGATGCCGTGCTCATCGACGACAGTCTCCCTGAAATGAGGC | 2470 |
| 2394 | Db | GANAACAGCCCGCTGAGGATGCCGTGCTCATCGACGAGTCTCCCTGAAATGAGGC | 2453 |
| 2471 | Qy | AGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACACGCGTGCGCATCAGG | 2530 |
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| 2531 | Qy | GGCAAGTCCCTACCTGCAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTC | 2590 |
| 2514 | Db | GGCAAGTCCCTACCTGCAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTC | 2573 |
| 2591 | Qy | TGCAGCCTGTGCTACGCGCAGATCGAGAAACAAGCTGTTTCGGGGATTCGGCGGACGGG | 2650 |
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| 2651 | Qy | CTGCTCCTCGGTTTGTGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCCACGCGAAA | 2710 |
| 2634 | Db | CTGCTCCTCGGTTTGTGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCCACGCGAAA | 2693 |
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| 2771 | Qy | AAGACAGTGTGAACCTCCCTGTAGAAGACGAGGCGCTGGGTGGACACGCTTTGTGTTACG | 2830 |
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| 3114 | Db | CATCAGCAAGTTTGGAGAACCCACATTTTTCCTGCGCGTCTATCTCTCACACGCGCTCC | 3173 |
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Db 3174 CTCTGCTACTCCTCTCTGAAAGCAAGACGACGAGGATGCTGCTGGGGCCCAAGGGCGCC 3233
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RESULT 14

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US-08-854-050-173
; Sequence 173, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOC/KET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..4029
; OTHER INFORMATION: /note= "preliminary sequence for
; OTHER INFORMATION: human TRF cDNA insert of
; OTHER INFORMATION: plasmid pGRN121"
; US-08-854-050-173
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Query Match 95.3%; Score 3618.6; DB 3; Length 4029;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;
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QY 13 GCAGCGCTCGTCTCTGCGACGTGGGAAGCCCTGGCCCGCCGCGGCGGCGGCGGCGGCGGCGGCGG 72
Db 1 GCAGCGCTCGTCTCTGCGACGTGGGAAGCCCTGGCCCGCCGCGGCGGCGGCGGCGGCGGCGGCGG 60
QY 73 GCGCGCTCCCGCTGCGGAGCGGTGCGTCCCTGCTGCGCGCCACTACCGGAGGTGCT 132
Db 61 GCGCGCTCCCGCTGCGGAGCGGTGCGTCCCTGCTGCGCGCCACTACCGGAGGTGCT 120
QY 133 GCGCGTGGCCACGTTCTGCGCGGCGCTGGGCGCCCGCAGGGCTGGCGGCTGGTGGCGGCGG 192
Db 121 GCGCGTGGCCACGTTCTGCGGCGGCGCTGGGCGCCCGCAGGGCTGGCGGCTGGTGGCGGCGG 180
QY 193 GGACCGCGCGGCTTCCGCGCGCTGCTGGGCGCCAGTGCCTGGTGGTGGTGGTGGTGGTGGTGGTGG 252
Db 181 GGACCGCGCGGCTTCCGCGCGTGGTGGCGCCANTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 253 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 312
Db 241 ANGCGNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 313 CCGAGTGTGCGAGAGGCTGTGCGGAGCGCGCGCGGGAAGACGTGCTGCGCTTCGCGCTTCGCGCTTCGC 372
Db 301 CCGAGTGTGCGANAGCTGTGCGGAGCGCGCGGGAAGACGTGCTGCGCTTCGCGCTTCGCGCTTCGC 360
QY 373 GCTGCTGGACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 432
Db 361 GCTGCTGGACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 433 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 492
Db 421 CCTGCCCAACACGCGTGACCGACGACTGCGGGGGAGCGGGGGCGTGGGGGCGTGGTGGTGGCG 480
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Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;

| | | | |
|----|------|--|------|
| QY | 13 | GCAGCGCTGGGTCTCTGCTGGCGACGTGGGAGCCCTGGCCCCGGCCACACCCCGCGATGCC | 72 |
| DB | 1 | GCAGCGTGGTCTCTGCTGGCGACGTGGGAGCCCTGGCCCCGGCCACCCCGCGATGCC | 60 |
| QY | 73 | GCGGCTCCCGCTGGCGAGCGGTGCGCTGCTGCTGGCGAGCCACATACCGCGAGTGCT | 132 |
| DB | 61 | GCGGCTCCCGCTGGCGAGCGGTGCGCTGCTGCTGGCGAGCCACATACCGCGAGTGCT | 120 |
| QY | 133 | GCCTCTGGCCACGTTCTGTGGCGGCCCTGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG | 192 |
| DB | 121 | GCCTCTGGCCACGTTCTGTGGCGGCCCTGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG | 180 |
| QY | 193 | GGACCCGGCGCTTTTCCGCGCGCTGGTGGCCAGTGGCTGGTGTGCGTGGCCCTGGGAGCG | 252 |
| DB | 181 | GGACCCGGCGCTTTTCCGCGCGTGGTGGCCAGTGGCTGGTGTGCGTGGCCCTGGGANGN | 240 |
| QY | 253 | ACGGCGCCCGCCGCGCCCTCTCTTCCGCGAGGTGTCTGTGCTGAAGGAGCTGGTGGC | 312 |
| DB | 241 | ANGCNGCCCCCGCCGCTCTTCTTCGCGACGTTCTCTGCTGCGAGCCACATACCGCGAGTGCT | 300 |
| QY | 313 | CCGAGTCTGCAGAGGCTGTGCGAGCGGCGCGCAAGACGTGCTGGCTTCGGCTTCGC | 372 |
| DB | 301 | CCGAGTCTGCANANGCTGTGCGANCGCGCGCAANACGTGTGGCTTCGGCTTCGC | 360 |
| QY | 373 | GCTGCTGGACGGGCGCGGGGCCCCCGAGGCTTCACCAACAGCGTGGCCAGCTA | 432 |
| DB | 361 | GCTGCTGGACGGGCGCGGGGCCCCCGAGGCTTCACCAACAGCGTGGCCAGCTA | 420 |
| QY | 433 | CTTGCCCAACACGGTGACGACGACATGCGGGGGAGCGGGGCTGTGCTGCTGCG | 492 |
| DB | 421 | CCTGCCCAACACGGTGACGACGACATGCGGGGGAGCGGGGCTGTGCTGCTGCG | 480 |
| QY | 493 | CCGCTGGGCGACGACGCTGTTCACTGCTGGCAGCTGGCGGCTCTTTGTGCTGGT | 552 |
| DB | 481 | CCGCTGGGCGACGACGCTGTTCACTGCTGGCAGCTGGCGGCTCTTTGTGCTGGT | 540 |
| QY | 553 | GGTCTCCAGCTTGCCTTACACAGTGTGCGGGCGCCGCTGTACACAGCTCGGCGCTGCCAC | 612 |
| DB | 541 | GGNTCCAGCTGGCTTACCANGTGTGCGGGCGCGCTGTACACAGCTCGGCGCTGCNAC | 600 |
| QY | 613 | TCAGGCCGGCGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGCG | 672 |
| DB | 601 | TCAGGCCGGCGCCCGCCACACGCTANTGGA-CCCGAANGCGTCTGGAT-CCAACGCGC | 658 |
| QY | 673 | CTGGAACATAGCGTCAAGGAGCGCGGCTCCCGCTGGGCTGCCAGCCCGGCTGGAG | 732 |
| DB | 659 | CTGGAACATAGCGTCAAGGAGCGCGGCTCCCGCTGGG-CTGCCAGCCCGGCTGGAG | 717 |
| QY | 733 | GAGCGCGGGGCGAGTCCACGCGAAGTCTGCCCTTGCCCAAGAGGCCAGGCGCTGGCG | 792 |
| DB | 718 | GAGCGCGGGCGAGTCCAGCGCAAGTCTGCCCTTGCCCAAGAGGCCAGGCGTGGCG | 777 |
| QY | 793 | TGCCCTTGAGCCGAGCGGACGCCGTTGGCGAGGGTCTCTGGGCCACCCGCGCAGGAC | 852 |
| DB | 778 | TGCCCTTGAGCCGAGCGGACGCCGTTGGCGAGGGTCTCTGGGCCACCCGCGCAGGAC | 837 |
| QY | 853 | CGCTGGACCGAGTCAACGTTCTCTGTGCTGCTACCTGCCAGACCCGCCGAAGAAGC | 912 |
| DB | 838 | GCCTGGACCGAGTCAACGTTCTCTGTGCTGCTACCTGCCAGACCCGCCGAAGAAGC | 897 |
| QY | 913 | CACCTCTTTGGAGGGTGGCTCTCTGGACCGCGCACTGCCACCCATCCGTGGGCGCGCA | 972 |
| DB | 898 | CACCTCTTTGGAGGGTGGCTCTCTGGACCGCGCACTGCCACCCATCCGTGGGCGCGCA | 957 |
| QY | 973 | GCACACCGCGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACGACGCTTGTC | 1032 |
| DB | 958 | GCACACCGCGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACGACGCTTGTC | 1016 |
| QY | 1033 | CCGGGTGACCGAGACCAAGCACTTCTCTACTCTCTAGGGCGACAAAGAGACAGTGGC | 1092 |
| DB | 1017 | CCGGGTGACCGAGACCAAGCACTTCTCTACTCTCTAGGGCGACAAAGAGACAGTGGC | 1074 |

| | | | |
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| QY | 1093 | GCCCTCTCTTCTACTC-AGCTCTCTGAGGCCAGCCTGACTGCGCTCGAGGCTCGTGG | 1155 |
| Db | 1075 | NCCCTCTCTCTACTCAATATATCTGAGGCCAGCCTGACTGCGTTCGGAGGTTCTG | 1134 |
| QY | 1152 | AGACATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAGCTCCCGCAGGTTGCCCGCC | 1211 |
| Db | 1135 | GAGACATCTTTCTGGTTCCAGGCTTGGATGCCA-GGATTCGCCAGGTTGCCCGCC | 1193 |
| QY | 1212 | TGCCCCAGCGCTACTTGGCAATGGGCCCTCTGTTTCTGGAGCTGCTTGGGAACACCGCG | 1271 |
| Db | 1194 | TGCCCCAGCGNATCTGGCAATGGGCCCTCTGTTTCTGGAGCTGCTTGGGAACACCGCG | 1253 |
| QY | 1272 | AGTGCCCTACGGGGTCTCTCAAGACGACACTCCCGCTGCGAGCTGCGGTCACCCAG | 1331 |
| Db | 1254 | AGTGCCCTACGGGGTGTCTCAAGACGACACTCCCGCTGCGAGCTGCGGTCACCCAG | 1313 |
| QY | 1332 | CAGCGGTGTCTGTGCCGGGAGAACCCAGGGCTCTGTGGGGCCCCCGAGGAGG | 1391 |
| Db | 1314 | CAGCGGTGTCTGTGCCGGGAGAACCCAGGGCTCTGTGGGGCCCCCGAGGAGG | 1373 |
| QY | 1392 | -ACACAGACCCCTCGCTGGTGCGACTGCTCGCCACGACACAGCCCTTGGCAGGTG | 1450 |
| Db | 1374 | AACACAGACCCCTCGCTGGTGCGACTGCTCGCCACGACACAGCCCTTGGCAGGTG | 1433 |
| QY | 1451 | TACGGCTTGTGCGGGCTGCTCGCGCGGCTGTGTGCCCGCCAGGCCCTCGGGCTCCAGG | 1510 |
| Db | 1434 | TACGGCTTGTGCGGGCTGCTCGCGCGGCTGTGTGCCCGCCAGGCCCTCGGGCTCCAGG | 1493 |
| QY | 1511 | CACAAGACGCCCTTCTCAGGAACACCAAGAAGTTCTATCTCCCTGGGGAAGCATGCC | 1570 |
| Db | 1494 | CACAAGACGCCCTTCTCAGGAACACCAAGAAGTTCTATCTCCCTGGGGAAGCATGCC | 1553 |
| QY | 1571 | AAGCTCTCGTGCAGGAGCTGAGTGGAAATGAGCTGCGGAGCTGCGCTTGGCTGCCG | 1630 |
| Db | 1554 | AAGCTCTCGTGCAGGAGCTGAGTGGAAATGAGCTGCGGAGCTGCGCTTGGCTGCCG | 1613 |
| QY | 1631 | AGGAGCCGAGGGTTGCTGTGTTCCGGCCGACAGCAGCCGTCTGCTGAGGAGATCCTG | 1690 |
| Db | 1614 | AGGAGCCGAGGGTTGCTGTGTTCCGGCCGACAGCAGCCGTCTGCTGAGGAGATCCTG | 1673 |
| QY | 1691 | GCGAAGTTCCTGCACTGGCTGATGAGTGTAGTCTGTCGAGCTGCTCAGGTCCTTCTTT | 1750 |
| Db | 1674 | GCGAAGTTCCTGCACTGGCTGATGAGTGTAGTCTGTCGAGCTGCTCAGGTCCTTCTTT | 1733 |
| QY | 1751 | TATGTCAGGAGCACCGTTTCAAAGAACAGGGCTTTTCTACCGGAAGAGTGTCTGG | 1810 |
| Db | 1734 | TATGTCAGGAGCACCGTTTCAAAGAACAGGGCTTTTCTACCGGAAGAGTGTCTGG | 1793 |
| QY | 1811 | AGCAAGTTGCAAGCATTTGNAATCAGACAGCACTTGAAGAGGTGCAAGTTCGGGAGCTG | 1870 |
| Db | 1794 | AGCAAGTTGCAAGCATTTGNAATCAGACAGCACTTGAAGAGGTGCAAGTTCGGGAGCTG | 1853 |
| QY | 1871 | TCGGAAGCAGAGGTCAGGACATCTCGGAAGCCAGGCCCGCTGCTGAGCTCCAGACTC | 1930 |
| Db | 1854 | TCGGAAGCAGAGGTCAGGACATCTCGGAAGCCAGGCCCGCTGCTGAGCTCCAGACTC | 1913 |
| QY | 1931 | CGCTTCATCCCCAAGCTGACGGGCTCGGCCGATGTGAACATGGACTACGTCGTGGGA | 1990 |
| Db | 1914 | CGCTTCATCCCCAAGCTGACGGGCTCGGCCGATGTGAACATGGACTACGTCGTGGGA | 1973 |
| QY | 1991 | GCCAGACGTTCCGACAGAAAGAGGGCGGAGGCTCTCACTCGAGGTTGAAGGCACTG | 2050 |
| Db | 1974 | GCCAGACGTTCCGACAGAAAGAGGGCGGAGGCTCTCACTCGAGGTTGAAGGCACTG | 2033 |
| QY | 2051 | TTACGCGTGTCAACTACGAGCGGGCGGGCGCCCGGCTCTTGGGCGCTCTGTGCTG | 2110 |
| Db | 2034 | TTACGCGTGTCAACTACGAGCGGGCGGGCGCCCGGCTCTTGGGCGCTCTGTGCTG | 2093 |
| QY | 2111 | GGCTTGACGATATCCACAGGGCTGGCGACCTTCGTGCTGTGTGCGTGGGCCCCAGGAC | 2170 |
| Db | 2094 | GGCTTGACGATATCCACAGGGCTGGCGACCTTCGTGCTGTGTGCGTGGGCCCCAGGAC | 2153 |

QY 2171 CCGCGCCCTGAGCTGACTTTGTCAGAGTGGATGTGACGGGCGCGCTACGACACCATCCCC 2230
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Db 2154 CCGCCGCCCTGAGCTGACTTTGTCAAGTGGATGTGACGGGCGCGCTACGACACCATCCCC 2213
|||||
QY 2231 CAGGACAGGCTCAGGAGGTCTATCGCGACGATCATCAAAACCCAGAACACGTAAGTCCGCTG 2290
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Db 2214 CAGGACAGGCTCAGGAGGTCTATCGCGACGATCATCAAAACCCAGAACACGTAAGTCCGCTG 2273
|||||
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|||||
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QY 2351 CAGGCTCTACCTTGACACACCTCCAGCGGTACATCGGACAGTTCGTGGCTCAGCTGCAG 2410
|||||
Db 2334 CAGGCTCTACCTTGACACACCTCCAGCGGTACATCGGACAGTTCGTGGCTCAGCTGCAG 2393
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QY 2411 GAGACAGCCCGCTGAGGATGCCGTCGTCATCGAGCAGAGTCCCTCCCTGAATGAGGC 2470
|||||
Db 2394 GANACAGCCCGCTGAGGATGCCGTCGTCATCGAGCAGAGTTCCTCCCTGAATGAGGC 2453
|||||
QY 2471 AGCAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCCACACGCGGTGGGCAATCAGG 2530
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Db 2454 AGCAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCCACACGCGGTGGGCAATCAGG 2513
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QY 2531 GGCAGTCCCTAGTCCAGTCCAGGATCCGCGAGGCTCCATCCTCTCCAGCTGCTC 2590
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QY 2591 TGCAGGCTGTGTCAGGCGACATGGAGAACAGCTGTTTGGGGGATTCGGGGACGGG 2650
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QY 3071 TACAAGATCCTCTGTCAGGCGTACAGGTTTACGGCATGTGCTGAGCTCCCATTT 3130
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Db 3054 TACAAGATCCTCTGTCAGGCGTACAGGTTTACGGCATGTGCTGAGCTCCCATTT 3113
|||||
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|||||
QY 3431 GCACTGCCCTCAGACTTCAAGACCATCTTGGAATGATGGCCACCCGCCACAGCCAGGCC 3490
|||||
Db 3414 GCACTGCCCTCAGACTTCAAGACCATCTTGGAATGATGGCCACCCGCCACAGCCAGGCC 3473
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QY 3491 GAGAGCAGACACAGCAGCCCTGTCTACGCCGGGCTCTACGTCCAGGGAGGGAGGGCGG 3550
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QY 3791 CCCCTGAT 3798
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Search completed: October 7, 2003, 08:40:04
Job time : 213.841 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2003, 08:32:46 ; Search time 214.058 Seconds
(without alignments)
10736.958 Million cell updates/sec

Title: US-08-951-733-13_COPY_1920_2820

Perfect score: 901

Sequence: 1 GTCCAGACTCCGCTCATCC.....AGGCCCTGGTGGCAGCGCT 901

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

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- 2: /cgn2.6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 16: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 901 | 100.0 | 1314 | 14 | US-10-294-778-9 |
| 2 | 901 | 100.0 | 1866 | 14 | US-10-294-778-11 |
| 3 | 901 | 100.0 | 3396 | 10 | US-09-749-728B-32 |
| 4 | 901 | 100.0 | 3453 | 14 | US-10-205-629-1 |
| 5 | 901 | 100.0 | 4015 | 9 | US-09-733-294A-3 |
| 6 | 901 | 100.0 | 4015 | 10 | US-09-990-080-1 |
| 7 | 901 | 100.0 | 4015 | 10 | US-09-843-676-224 |
| 8 | 901 | 100.0 | 4015 | 10 | US-09-953-052-1 |
| 9 | 901 | 100.0 | 4015 | 14 | US-10-053-758-224 |
| 10 | 901 | 100.0 | 4015 | 14 | US-10-208-243-1 |
| 11 | 901 | 100.0 | 4015 | 14 | US-10-054-295-224 |
| 12 | 901 | 100.0 | 4015 | 14 | US-10-054-611-224 |
| 13 | 901 | 100.0 | 4015 | 14 | US-10-105-963-1 |
| 14 | 901 | 100.0 | 4015 | 14 | US-10-044-692-1 |
| 15 | 901 | 100.0 | 4015 | 14 | US-10-044-539-1 |
| 16 | 901 | 100.0 | 8742 | 12 | US-10-105-616-6 |

c

ALIGNMENTS

RESULT 1

US-10-294-778-9
; Sequence 9, Application US/10294778
; Publication No. US20030060417A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: NO. US20030060417A1e1 Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/10/294,778
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/582,924
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 9
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-294-778-9

Query Match 100.0%; Score 901; DB 14; Length 1314;

Best Local Similarity 100.0%; Pred No. 5,7e-242;

Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 324 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTCGCGCGGATTTGTGAACATGGACTA 383

QY 61 CGTCGTGGAGGCCAGAACGTTCCGCAGAGAAAGAGGCCGCGTCTCACCTCGAGGTT 120

Db 384 CGTCTGGGAGCCAGAACGTTCCGACAGAAAAGAGGGCCGAGGGTCTACCTCGAGGGT 443
Qy 121 GAAGGCACTGTTACAGCTGTCTCAACTACGAGCGGGCGGGCGCCCGCCGCTCTCTGGCGC 180
Db 444 GAAGGCACTGTTACAGCTGTCTCAACTACGAGCGGGCGGGCGCCCGCCGCTCTCTGGCGC 503
Qy 181 CTCTGTGCTGGGCTTGACGATATCCACAGGGCTGCGGACCTTCCTGCTGCTGTGGG 240
Db 504 CTCTGTGCTGGGCTTGACGATATCCACAGGGCTGCGGACCTTCCTGCTGCTGTGGG 563
Qy 241 GGCCAGAGCCCGCGCTGAGCTGTACTTGTCAAGGTGATGACGGCGGTACGA 300
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Qy 301 CACATCCCCAGGACAGGTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 360
Db 624 CACATCCCCAGGACAGGTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 683
Qy 361 GTACTGCTGGTGGTATCGGCTGCTGAGCTGTACTTGTCAAGGTGATGACGGCGGTACGA 420
Db 684 GTACTGCTGGTGGTATCGGCTGCTGAGCTGTACTTGTCAAGGTGATGACGGCGGTACGA 743
Qy 421 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCGGTACATGCGAGTTCGTGGC 480
Db 744 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCGGTACATGCGAGTTCGTGGC 803
Qy 481 TCACCTCGAGGACAGGTCAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 540
Db 804 TCACCTCGAGGACAGGTCAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 863
Qy 541 GAATGAGGCGGCTGCTCTGAGCTGTCTTGTGAGTATGAGTTCCTGAGTTCCTGAGTTC 600
Db 864 GAATGAGGCGGCTGCTCTGAGCTGTCTTGTGAGTATGAGTTCCTGAGTTCCTGAGTTC 923
Qy 601 GCGCATCAGGGGCAAGTCTTACCTTGACAGACCTCCAGCGGTACATCAAAACCCAGAACAC 660
Db 924 GCGCATCAGGGGCAAGTCTTACCTTGACAGACCTCCAGCGGTACATCAAAACCCAGAACAC 683
Qy 661 CAGCTCTCTGACGCTGTGCTACGCGGACATGAGAAAGCTGTTTGGGGGATTCG 720
Db 984 CAGCTCTCTGACGCTGTGCTACGCGGACATGAGAAAGCTGTTTGGGGGATTCG 1043
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Db 1224 T 1224

RESULT 2
US-10-294-778-11
; Sequence 11, Application US/10294778
; Publication No. US20030060417A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. US20030060417A1e1 Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/10/294, 778
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/582,924
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08

; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-294-778-11

Query Match 100.0%; Score 901; DB 14; Length 1866;
Best Local Similarity 100.0%; Pred. No. 6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCAGACTCGGCTTCATCCCAAGCCTGAGGGCTGCGGCCGATTTGTGAACATGACTA 60
Db 324 GTCAGACTCGGCTTCATCCCAAGCCTGAGGGCTGCGGCCGATTTGTGAACATGACTA 383
Qy 61 CGTCTGGGAGCCAGAACGTTCCCGAGAGAAAAGAGGGCCGAGGCTCTACCTCGAGGGT 120
Db 384 CGTCTGGGAGCCAGAACGTTCCCGAGAGAAAAGAGGGCCGAGGCTCTACCTCGAGGGT 443
Qy 121 GAAGGCACTGTTACAGCTGTCTCAACTACGAGCGGGCGGGCGCCCGCTCTCTGGCGC 180
Db 444 GAAGGCACTGTTACAGCTGTCTCAACTACGAGCGGGCGGGCGCCCGCTCTCTGGCGC 503
Qy 181 CTCTGTCTGGGCTTGACGATATCCACAGGGCTGCGGACCTTCGCTGCTGTGGTGGC 240
Db 504 CTCTGTCTGGGCTTGACGATATCCACAGGGCTGCGGACCTTCGCTGCTGTGGTGGC 563
Qy 241 GGCCAGAGCCCGCGCTGAGCTGTACTTGTCAAGGTGATGAGGGCGGTACGA 300
Db 564 GGCCAGAGCCCGCGCTGAGCTGTACTTGTCAAGGTGATGAGGGCGGTACGA 623
Qy 301 CACATCCCCAGGACAGGTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 360
Db 624 CACATCCCCAGGACAGGTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 683
Qy 361 GTACTGCTGGCTCGGTATGCGGTGTCAGAGGGCCGCCATGGGACGTCGCAAGGC 420
Db 684 GTACTGCTGGCTCGGTATGCGGTGTCAGAGGGCCGCCATGGGACGTCGCAAGGC 743
Qy 421 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCGGTACATGCGAGTTCGTGGC 480
Db 744 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCGGTACATGCGAGTTCGTGGC 803
Qy 481 TCACCTCGAGGACAGGTCAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 540
Db 804 TCACCTCGAGGACAGGTCAGGTCATCGCCAGCATCATCAAAACCCAGAACAC 863
Qy 541 GAATGAGGCGGCTGCTCTTCTGAGCTGTCTTCTTACGCTTCTATGTCGACACGCGGT 600
Db 864 GAATGAGGCGGCTGCTCTTCTGAGCTGTCTTCTTACGCTTCTATGTCGACACGCGGT 923
Qy 601 GCGCATCAGGGGCAAGTCTTACCTTGACAGGTCATCGCCAGGGATCCCGAGGGCTTCATCTCTC 660
Db 924 GCGCATCAGGGGCAAGTCTTACCTTGACAGGTCATCGCCAGGGATCCCGAGGGCTTCATCTCTC 983
Qy 661 CAGCTCTCTGACGCTGTGCTACGCGGACATGAGAAAGCTGTTTGGGGGATTCG 720
Db 984 CAGCTCTCTGACGCTGTGCTACGCGGACATGAGAAAGCTGTTTGGGGGATTCG 1043
Qy 721 GCGGACGGGCTGCTCTGCGGCTTGTGAGTATTTCTTGTGAGTTCCTGAGTTCCTGAGTTC 780
Db 1044 GCGGACGGGCTGCTCTGCGGCTTGTGAGTATTTCTTGTGAGTTCCTGAGTTCCTGAGTTC 1103
Qy 781 CCAGCGAAAACCTTCTCAGGACCTTGTGCGAGGTCCTGAGTTCCTGAGTTCCTGAGTTC 840
Db 1224 T 1224

Db 1104 CCACGCGAAACCTTCTCCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGT 1163
QY 841 GAACCTGGGAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGC 900
Db 1164 GAACCTGGGAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGC 1223
QY 901 T 901
Db 1224 T 1224

RESULT 3
US-09-749-728B-32
; Sequence 32, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-Ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749,728B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 32
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: (1)..(3399)
US-09-749-728B-32

Query Match 100.0%; Score 901; DB 10; Length 3396;
Best Local Similarity 100.0%; Pred. No. 6.5e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCGGATGTGAACATGGACTA 60
Db 1854 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCGGATGTGAACATGGACTA 1913
QY 61 CGCTGGGAGGACAGACCTTCGCGAGAGAAAGAGGCGGCGGCTCTCACCTCAGAGGT 120
Db 1914 CGTGTGGGAGGACAGACCTTCGCGAGAGAAAGAGGCGGCGGCTCTCACCTCAGAGGT 1973
QY 121 GAAGGACTGTTACGGTCTCACTACAGCGGGGCGGCGGCGGCGGCTCTCTGGGCGC 180
Db 1974 GAAGGACTGTTACGGTCTCACTACAGCGGGGCGGCGGCGGCGGCTCTCTGGGCGC 2033
QY 181 CTTCTGTGTGGGCTTGGAGGATATCCACAGGGGCTTGGCGACCTTCGTGCTGGGTGGG 240
Db 2034 CTTCTGTGTGGGCTTGGAGGATATCCACAGGGGCTTGGCGACCTTCGTGCTGGGTGGG 2093
QY 241 GGCCAGGACCGCGGCTTGGAGTGTACTTTGTCAAGTGGATGTGACGGGCGGCTACGA 300
Db 2094 GGCCAGGACCGCGGCTTGGAGTGTACTTTGTCAAGTGGATGTGACGGGCGGCTACGA 2153
QY 301 CACCATCCCCAGGACAGGCTCACGGAGGTATCGCCAGCATCATCAAACCCAGAACAC 360
Db 2154 CACCATCCCCAGGACAGGCTCACGGAGGTATCGCCAGCATCATCAAACCCAGAACAC 2213
QY 361 GTACTGCGTGGCTGCGTATGCCGTGTCCAGAAAGGCGGCGGCTTGGCGACGCTCCGCAAGGC 420

Db 2214 GTACTGCGTGGTGGTATGCCGTGTCAGAAAGCCGCCATGGGACGCTCCGCAAGGC 2273
QY 421 CTTCAAGACCCACGCTCTTACCTTGACAGACCTCCAGCCGCTACATCCGACAGTTCGTGGC 480
Db 2274 CTTCAAGACCCACGCTCTTACCTTGACAGACCTCCAGCCGCTACATCCGACAGTTCGTGGC 2333
QY 481 TCACCTGCAGGAGACGACCCCGCTGAGGATGCCGTGCTCATCGAGACAGCTTCCTCCCT 540
Db 2334 TCACCTGCAGGAGACGACCCCGCTGAGGATGCCGTGCTCATCGAGACAGCTTCCTCCCT 2393
QY 541 GAATGAGGCGACGAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCGACACGACCGCT 600
Db 2394 GAATGAGGCGACGAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCGACACGACCGCT 2453
QY 601 GCGCATCAGGGCAAGTCTCTACGTCCAGTCCAGGGGATCCGCGAGGGCTCCATCTCTCTC 660
Db 2454 GCGCATCAGGGCAAGTCTCTACGTCCAGTCCAGGGGATCCGCGAGGGCTCCATCTCTCTC 2513
QY 661 CACGCTGCTTCGACGCTGTGTACGGCGACATGGAGAACAGCTGTTTGGCGGGATTGG 720
Db 2514 CACGCTGCTTCGACGCTGTGTACGGCGACATGGAGAACAGCTGTTTGGCGGGATTGG 2573
QY 721 GCGGGAAGGGCTGCTCTCGCTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCAC 780
Db 2574 GCGGGAAGGGCTGCTCTCGCTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCAC 2633
QY 781 CCACGCGAAACCTTCTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGTGCCTGGT 840
Db 2634 CCACGCGAAACCTTCTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGTGCCTGGT 2693
QY 841 GAACCTGGGAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCGCTGGGTGGCAGGC 900
Db 2694 GAACCTGGGAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCGCTGGGTGGCAGGC 2753
QY 901 T 901
Db 2754 T 2754

RESULT 4
US-10-205-629-1
; Sequence 1, Application US/10205629
; Publication No. US20030049236A1
; GENERAL INFORMATION:
; APPLICANT: Kassem, Moustapha
; APPLICANT: Jensen, Thomas
; APPLICANT: Rattan, Suresh
; TITLE OF INVENTION: Immortalized Stem Cells
; FILE REFERENCE: 006148.00002
; CURRENT APPLICATION NUMBER: US/10/205,629
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 60/315939
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PA 2001 01148
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-629-1
Query Match 100.0%; Score 901; DB 14; Length 3453;
Best Local Similarity 100.0%; Pred. No. 6.5e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCGGATTTGTGAACATGGACTA 60
Db 1863 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCGGATTTGTGAACATGGACTA 1922
QY 61 CGTGTGGGAGGACGACGCTTCGCGAGAGAAAGAGGCGGCGGCTCTCACCTCGAGGCT 120

Db 1923 CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGCGAGCGTCTACCTCGAGGGT 1982
Qy 121 GAAGGCACTGTTGAGCGTGTCTCAACTACGAGCGGCGCGCGCCCGCTCTCTGGGCGC 180
Db 1983 GAAGGCACTGTTGAGCGTGTCTCAACTACGAGCGGCGCGCGCCCGCTCTCTGGGCGC 2042
Qy 181 CTCTGTGCTGGGCTGGACGATFCCACAGGGCTGGCGACCTTCGTGTGCTGTGCG 240
Db 2043 CTCTGTGCTGGGCTGGACGATFCCACAGGGCTGGCGACCTTCGTGTGCTGTGCG 2102
Qy 241 GGGCCAGGACCCGCGCTGAGCTGACTTGTTCAGGTTGATGTGAGCGGCGGCTACGA 300
Db 2103 GGGCCAGGACCCGCGCTGAGCTGACTTGTTCAGGTTGATGTGAGCGGCGGCTACGA 2162
Qy 301 CACCATCCCCCAGGACAGCGTTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAC 360
Db 2163 CACCATCCCCCAGGACAGCGTTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAC 2222
Qy 361 GTACTGCGTGGCTGGTATGCCGTGTCCAGAGGCGCCCATGGGCACGTCCGCAAGGC 420
Db 2223 GTACTGCGTGGCTGGTATGCCGTGTCCAGAGGCGCCCATGGGCACGTCCGCAAGGC 2282
Qy 421 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGGCAGATTCGTGGC 480
Db 2283 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGGCAGATTCGTGGC 2342
Qy 481 TCACCTCGAGGAGACCAAGCGGCTGAGGGATGCGTCTCATGAGCAGAGCTCCCTCCCT 540
Db 2343 TCACCTCGAGGAGACCAAGCGGCTGAGGGATGCGTCTCATGAGCAGAGCTCCCTCCCT 2402
Qy 541 GAATGAGGCGAGAGTGGCTCTTTCGACGTCTTCTTACGCTTCATGTCGCCACACGCGT 600
Db 2403 GAATGAGGCGAGAGTGGCTCTTTCGACGTCTTCTTACGCTTCATGTCGCCACACGCGT 2462
Qy 601 GCGCATCAGGGGAGAGTCCCTACGTCAGTCCAGTCCGAGGGATCCCGAGGGCTCCATCCCTC 660
Db 2463 GCGCATCAGGGGAGAGTCCCTACGTCAGTCCGAGGGATCCCGAGGGCTCCATCCCTC 2522
Qy 661 CACGCTGCTTGACGCTGTGCTACGCGACATGGAGAACAGCTGTTTGGGGGATTCG 720
Db 2523 CACGCTGCTTGACGCTGTGCTACGCGACATGGAGAACAGCTGTTTGGGGGATTCG 2582
Qy 721 GCGGAGCGGCTGCTCCTGCGTGTGGTGGATGATTTCTTGTGGTGACACCTCACCTCAC 780
Db 2583 GCGGAGCGGCTGCTCCTGCGTGTGGTGGATGATTTCTTGTGGTGACACCTCACCTCAC 2642
Qy 781 CCAGCGGAAACCTTCTCAGGACCTGTCAGGACCTGTCGAGGTGTCCTGAGTATGGCTGCGTGGT 840
Db 2643 CCAGCGGAAACCTTCTCAGGACCTGTCAGGACCTGTCGAGGTGTCCTGAGTATGGCTGCGTGGT 2702
Qy 841 GAACTTGGGGAAGACAGTGTGAACTTCCCTGTAGAGAGAGGCGCCCTGGGTGGCAGGCG 900
Db 2703 GAACTTGGGGAAGACAGTGTGAACTTCCCTGTAGAGAGAGGCGCCCTGGGTGGCAGGCG 2762
Qy 901 T 901
Db 2763 T 2763

RESULT 5
US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)....(3454)
US-09-733-294A-3

Query Match 100.0%; Score 901; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCAGACTCGCTTCATCCCAAGCCTGAGGGCTGGGCCGATTTGTAACATGGACTA 60
Db 1909 GTCAGACTCGCTTCATCCCAAGCCTGAGGGCTGGGCCGATTTGTAACATGGACTA 1968
Qy 61 CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGCGGAGCGTCTCACCTCGAGGT 120
Db 1969 CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGCGGAGCGTCTCACCTCGAGGT 2028
Qy 121 GAAGGCACTGTTACGCGTGTCTCAACTACGAGCGGCGCGCGCCCGCTCTCTGGGCGC 180
Db 2029 GAAGGCACTGTTACGCGTGTCTCAACTACGAGCGGCGCGCGCCCGCTCTCTGGGCGC 2088
Qy 181 CTCTGTCTGGGCTTGACGATATCCACAGGGCTGGCGACCTTCGTGTGCTGTGGC 240
Db 2089 CTCTGTCTGGGCTTGACGATATCCACAGGGCTGGCGACCTTCGTGTGCTGTGGC 2148
Qy 241 GGGCCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGGTACGA 300
Db 2149 GGGCCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGGTACGA 2208
Qy 301 CACATCCCCAGAGACAGGCTCACGAGGTATCCGCCAGCATATCAAAACCCAGAACAC 360
Db 2209 CACATCCCCAGAGACAGGCTCACGAGGTATCCGCCAGCATATCAAAACCCAGAACAC 2268
Qy 361 GTACTGCGTGGTGGTATGCCGTGGTCCAGAAAGCGCCCATGGGCACGTCCGCAAGGC 420
Db 2269 GTACTGCGTGGTGGTATGCCGTGGTCCAGAAAGCGCCCATGGGCACGTCCGCAAGGC 2328
Qy 421 CTTCAAGAGCACGCTCTTACCTTGACAGACTCCAGCGTACATGCGACAGTTCTGGC 480
Db 2329 CTTCAAGAGCACGCTCTTACCTTGACAGACTCCAGCGTACATGCGACAGTTCTGGC 2388
Qy 481 TCACCTCGAGAGACCAAGCGCTGAGGGATGCCGTCTCATCAGAGCAGAGCTCCTCCCT 540
Db 2389 TCACCTCGAGAGACCAAGCGCTGAGGGATGCCGTCTCATCAGAGCAGAGCTCCTCCCT 2448
Qy 541 GAATGAGGCGAGTGGCTCTTCGACGCTTCCTACGCTTCATGTCGACACAGCGGT 600
Db 2449 GAATGAGGCGAGTGGCTCTTCGACGCTTCCTACGCTTCATGTCGACACAGCGGT 2508
Qy 601 GCGCATCAGGGGCAAGTCCCTACGTCAGTGCAGGGATCCCGAGGGCTCCATCCCTC 660
Db 2509 GCGCATCAGGGGCAAGTCCCTACGTCAGTGCAGGGATCCCGAGGGCTCCATCCCTC 2568
Qy 661 CACGCTCTGACGCTGTGCTACGCGCATGAGGAACAGCTGTTTGGGGGATTCG 720
Db 2569 CACGCTCTGACGCTGTGCTACGCGCATGAGGAACAGCTGTTTGGGGGATTCG 2628
Qy 721 GCGGAGCGGCTGCTCCTGCGTGTGGTGGATTTCTTGTGTGACACCTCACCTCAC 780
Db 2629 GCGGAGCGGCTGCTCCTGCGTGTGGTGGATTTCTTGTGTGACACCTCACCTCAC 2688
Qy 781 CCAGCGGAAACCTTCTCAGGACCTTGGTCCGAGGTGTCCTCAGTATGGCTCGGTGGT 840
Db 2689 CCAGCGGAAACCTTCTCAGGACCTTGGTCCGAGGTGTCCTCAGTATGGCTCGGTGGT 2748
Qy 841 GAACTTGGGGAAGACAGTGGTGAACCTTCCCTGTAGAGAGAGGCGCCCTGGGTGGCAGGCG 900

|||||
Db 2749 GAATGCGGAGACAGTGGTGAATCTCCCTGAGAGAGAGGCGCTGGTGGACAGGC 2808
QY 901 T 901
Db 2809 T 2809
RESULT 6
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258c
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1
Query Match 100.0%; Score 901; DB 10; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATGTGAACATGGACTA 60
Db 1909 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATGTGAACATGGACTA 1968
QY 61 CGTCGTGGGAGCCAGACAGCTTCCGAGAGAAAGAGGCGCGAGCGCTCACCTCGAGGGT 120
Db 1969 CGTCGTGGGAGCCAGACAGCTTCCGAGAGAAAGAGGCGCGAGCGCTCACCTCGAGGGT 2028
QY 121 GAAGGACTGTTCAGCGTGTCTCACTACAGAGCGGCGCGGCCCGCCGCTCTCGGGCGC 180
Db 2029 GAAGGACTGTTCAGCGTGTCTCACTACAGAGCGGCGCGGCCCGCCGCTCTCGGGCGC 2088
QY 181 CTCTGTGCTGGGCTGGAGGATATCCACAGGCGCTGGCGCACCTTCGTGCTCGTGTGGC 240
Db 2089 CTCTGTGCTGGGCTGGAGGATATCCACAGGCGCTGGCGCACCTTCGTGCTCGTGTGGC 2148
QY 241 GCGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGCGTACGA 300
Db 2149 GCGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGCGTACGA 2208
QY 301 CACCAATCCCGCCAGGACAGGCTCACGAGGTATCGCCAGCATCATCAAAACCCAGAACAC 360
Db 2209 CACCAATCCCGCCAGGACAGGCTCACGAGGTATCGCCAGCATCATCAAAACCCAGAACAC 2268
QY 361 GTACTGCGTGGCTGCGTATCGGCTGGTCCAGAGCGCCGATGGCAGCTCCGCAAGGC 420
Db 2269 GTACTGCGTGGCTGCGTATCGGCTGGTCCAGAGCGCCGATGGCAGCTCCGCAAGGC 2328
QY 421 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCGGTATCATGCGACAGTTCGTGGC 480
Db 2329 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCGGTATCATGCGACAGTTCGTGGC 2388
QY 481 TCACCTGCAGGAGACACCGCCGCTGAGGATCCCGCTCGTTCATCGAGCAGAGCTCCCTCC 540
Db 2389 TCACCTGCAGGAGACACCGCCGCTGAGGATCCCGCTCGTTCATCGAGCAGAGCTCCCTCC 2448

QY 541 GAATGAGCCAGCAGTGGCCTCTTCGACGCTTCTTCCATGCTTACGCTTCCATGCGCACACGCGCT 600
Db 2449 GAATGAGCCAGCAGTGGCCTCTTCGACGCTTCTTCCATGCTTACGCTTCCATGCGCACACGCGCT 2508
QY 601 GCGCATCAGGGGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCGCGAGGCTCCATCTCTC 660
Db 2509 GCGCATCAGGGGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCGCGAGGCTCCATCTCTC 2568
QY 661 CACGCTGCTCTGACGCTGTGTACGGCGACATGGAGAAACAAGCTTTTGGCGGGGATTCG 720
Db 2569 CACGCTGCTCTGACGCTGTGTACGGCGACATGGAGAAACAAGCTTTTGGCGGGGATTCG 2628
QY 721 GCGGGACGCGCTGCTCTGCTGCTTGGTGGATGATTTCTTGGTGGACACCTCACCTCAC 780
Db 2629 GCGGGACGCGCTGCTCTGCTGCTTGGTGGATGATTTCTTGGTGGACACCTCACCTCAC 2688
QY 781 CCACGGAAACCTTCTCAGGACCTGCTCAGGACCTGCTCAGGAGTGTCCCTGAGTATGGTGGT 840
Db 2689 CCACGGAAACCTTCTCAGGACCTGCTCAGGACCTGCTCAGGAGTGTCCCTGAGTATGGTGGT 2748
QY 841 GAACCTTGGGAGACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCGCTGGTGGCAGCGC 900
Db 2749 GAACCTTGGGAGACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCGCTGGTGGCAGCGC 2808
QY 901 T 901
Db 2809 T 2809
RESULT 7
US-09-843-676-224
; Sequence 224, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:


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;
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-003600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "human telomerase reverse
; transcriptase (hTERT)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1

Query Match 100.0%; Score 901; DB 10; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGCTGGCGCGATTGTGAACATGACTA 60
DB 1909 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGCTGGCGCGATTGTGAACATGACTA 1968
QY 61 CGTCGTGGAGCCAGAACCTTCCGAGAGAAAGAGCGCGAGCTCTCACCTCAGGGT 120
DB 1969 CGTCGTGGAGCCAGAACCTTCCGAGAGAAAGAGCGCGAGCTCTCACCTCAGGGT 2028
QY 121 GAAGGACATGTTACGCTGCTCAACTACAGAGCGGGCGGCGCCCGGCTCTCGGGGC 180
DB 2029 GAAGGACATGTTACGCTGCTCAACTACAGAGCGGGCGGCGCCCGGCTCTCGGGGC 2088
QY 181 CTCGTGTGGCCCTGGAGGATATCCACAGGSCCTGGCGCACTTCGTGCTCGGTGGC 240
DB 2089 CTCGTGTGGCCCTGGAGGATATCCACAGGSCCTGGCGCACTTCGTGCTCGGTGGC 2148
QY 241 GCGCCAGGACCCGCGCTGAGCTGCTACTTTGTCAAGTGGATGTGACGGCGCGTACGA 300
DB 2149 GCGCCAGGACCCGCGCTGAGCTGCTACTTTGTCAAGTGGATGTGACGGCGCGTACGA 2208
QY 301 CACCATCCCAAGGACAGGCTACGGAGGTATCCGCCAGCATCATCAACCCCAAGAAC 360
DB 2209 CACCATCCCAAGGACAGGCTACGGAGGTATCCGCCAGCATCATCAACCCCAAGAAC 2268
QY 361 GTACTGCGTGGCTCGGTATCGCGTGTCCAGAGCGCCCATGGSCAGCTCCGCAAGGC 420
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QY 541 GAATGAGCCAGCAGTGGCTCTTCGAGCTCTTCCTAGCTTCATGTGCCACAGCGCT 600
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QY 601 GCGCATGAGGGCAAGTCTTACGTCAGTGCAGGGGATCCGCGAGGGCTCCATCTCTC 660
DB 2509 GCGCATGAGGGCAAGTCTTACGTCAGTGCAGGGGATCCGCGAGGGCTCCATCTCTC 2568
QY 661 CAGCTGCTCTGCAGCCCTGTGTACGGGACATGAGAACAGCTGTTTGGGGGATTGG 720
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; Db 2629 GCGGACGGCTGCTCCTCGTTGGTGATGATTTCTTTGGTGACACCTCACTCAC 2688
; QY 781 CCACGCGAAACCTTCTCTCAGGACCTGCTCCGAGGTGTCCCTGAGTATGGCTGGTGT 840
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; QY 841 GAACCTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAGAGAGGCGCTGGTGGCAGCGC 900
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; Db 2809 T 2809
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; RESULT 9
; US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hprt"
; /note= "human telomerase reverse
; transcriptase (hprt) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224

Query Match      100.0%; Score 901; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCGCTTATCCCAAGCTGACGGGCTCGGCCGCGATGTGAACATGGACTA 60
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1909 GTCCAGACTCGCTTATCCCAAGCTGACGGGCTCGGCCGCGATGTGAACATGGACTA 1968
QY 61 CGTGTGGGAGCCAGAACGTTCCGACAGAAAAGAGGCGGAGCGTCTACCTCGAGGGT 120
Db
1969 CGTGTGGGAGCCAGAACGTTCCGACAGAAAAGAGGCGGAGCGTCTACCTCGAGGGT 2028
QY 121 GAAGGCACTGTTGAGCGTGTCTCAACTACGAGCGGCGCGGCCGCTCTCTGGGCGC 180
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2029 GAAGGCACTGTTGAGCGTGTCTCAACTACGAGCGGCGCGGCCGCTCTCTGGGCGC 2088
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QY 481 TCACCTGCAGGAGACACCGCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCT 540
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QY 661 CAGCGTCTCTGAGCGCTGTCGTACGCGGACATGGAGAACAAAGCTGTTTCGGGGGATTCG 720
Db
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QY 901 T 901

Query Match      100.0%; Score 901; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGTGTGGGAGCCAGAACGTTCCGACAGAAAAGAGGCGGAGCGTCTACCTCGAGGGT 120
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1969 CGTGTGGGAGCCAGAACGTTCCGACAGAAAAGAGGCGGAGCGTCTACCTCGAGGGT 2028
QY 121 GAAGGCACTGTTGAGCGTGTCTCAACTACGAGCGGCGCGGCCGCTCTCTGGGCGC 180
Db
2029 GAAGGCACTGTTGAGCGTGTCTCAACTACGAGCGGCGCGGCCGCTCTCTGGGCGC 2088
QY 181 CTCTGTGCTGGGCTTGACGATATCCACAGGCGTTCACCTCGAGGGT 240
Db
2089 CTCTGTGCTGGGCTTGACGATATCCACAGGCGTTCACCTCGAGGGT 2448
QY 241 GGCCAGAGCCCGCGCTTACCTTTCAGAGCTTCCAGGCGTATGACGGCGGTACGA 300
Db
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Db
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QY 781 CCACGGGAAAACCTTCTCAGGACCTTGGTCCAGAGTGTCCCTGAGTGATGGCTGCGGTGGT 840
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2689 CCACGGGAAAACCTTCTCAGGACCTTGGTCCAGAGTGTCCCTGAGTGATGGCTGCGGTGGT 2748
QY 841 GAACCTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAGAGCAGGCGCCCTGGGTGGCAGCGC 900
Db
2749 GAACCTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAGAGCAGGCGCCCTGGGTGGCAGCGC 2808
QY 901 T 901
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| | | | |
|--|------|---|------|
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| DB | 2449 | GAATGAGGCCAGCAGTGGCCCTCTTCGACGCTTCCTACGCTTCATGTGCCACACACGCCGT | 2508 |
| QY | 601 | GCGCATCAGGGGCAAGTCCCTACGCTCCAGTCCAGGGGATCCCGCAGGGCTCCCATCCTCTC | 660 |
| DB | 2509 | GCGCATCAGGGGCAAGTCCCTACGCTCCAGTCCAGGGGATCCCGCAGGGCTCCCATCCTCTC | 2568 |
| QY | 661 | CACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTCGCGGGGATTCG | 720 |
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| QY | 721 | CGCGGACGGGCTGCTCTCTGGCTTGGTGGATGATTTCTTGGTGACACCTCACCTCAC | 780 |
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| QY | 781 | CCACGCGAAACCTTCTCAGGACCTTGGTCCAGGCTGTCCTCCAGTATGATGGCTGCGTGGT | 840 |
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| QY | 841 | GAATTCGCGGAACAGCAGTGGTGAACTTCCTCTGTAGAACAGAGGCCCTGGGTGGCACGGC | 900 |
| DB | 2749 | GAATTCGCGGAACAGCAGTGGTGAACTTCCTCTGTAGAACAGAGGCCCTGGGTGGCACGGC | 2808 |
| QY | 901 | T 901 | |
| DB | 2809 | T 2809 | |
| RESULT 11 | | | |
| US-10-054-295-224 | | | |
| ; Sequence 224, Application US/10054295 | | | |
| ; Publication No. US20030044953A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Cech, Thomas R. | | | |
| ; Lingner, Joachim | | | |
| ; Nakamura, Toru | | | |
| ; Chapman, Karen B. | | | |
| ; Morin, Gregg B. | | | |
| ; Harley, Calvin | | | |
| ; Andrews, William H. | | | |
| ; TITLE OF INVENTION: No. US20030044953A1el Telomerase | | | |
| ; NUMBER OF SEQUENCES: 225 | | | |
| ; CORRESPONDENCE ADDRESS: | | | |
| ; ADDRESSEE: Townsend and Townsend and Crew LLP | | | |
| ; STREET: Two Embarcadero Center, 8th Floor | | | |
| ; CITY: San Francisco | | | |
| ; STATE: California | | | |
| ; COUNTRY: United States of America | | | |
| ; ZIP: 94111 | | | |
| ; COMPUTER READABLE FORM: | | | |
| ; MEDIUM TYPE: Floppy disk | | | |
| ; COMPUTER: IBM PC compatible | | | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| ; SOFTWARE: Patentin Release #1.0, Version #1.30 | | | |
| ; CURRENT APPLICATION DATA: | | | |
| ; APPLICATION NUMBER: US/10/054,295 | | | |
| ; FILING DATE: 18-Jan-2002 | | | |
| ; CLASSIFICATION: 536 | | | |
| ; PRIOR APPLICATION DATA: | | | |
| ; APPLICATION NUMBER: 08/854,050 | | | |
| ; FILING DATE: <Unknown> | | | |
| ; APPLICATION NUMBER: US 08/846,017 | | | |
| ; FILING DATE: 25-APR-1997 | | | |
| ; APPLICATION NUMBER: US 08/844,419 | | | |
| ; FILING DATE: 18-APR-1997 | | | |
| ; APPLICATION NUMBER: US 08/724,643 | | | |
| ; FILING DATE: 01-OCT-1996 | | | |
| ; ATTORNEY/AGENT INFORMATION: | | | |
| ; NAME: Apple, Randolph T. | | | |
| ; REGISTRATION NUMBER: 36,429 | | | |
| ; REFERENCE/DOCKET NUMBER: 015389-002930US | | | |

| | | | | | | | | | |
|--------------------------------|--|--|--------------|---------------|------------|-----|--------|-------|------|
| TELECOMMUNICATION INFORMATION: | | | | | | | | | |
| ; | TELEPHONE: (415) 576-0200 | | | | | | | | |
| ; | TELEFAX: (415) 576-0300 | | | | | | | | |
| ; | INFORMATION FOR SEQ ID NO: 224: | | | | | | | | |
| ; | SEQUENCE CHARACTERISTICS: | | | | | | | | |
| ; | LENGTH: 4015 base pairs | | | | | | | | |
| ; | TYPE: nucleic acid | | | | | | | | |
| ; | STRANDEDNESS: single | | | | | | | | |
| ; | TOPOLOGY: linear | | | | | | | | |
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| ; | FEATURE: | | | | | | | | |
| ; | NAME/KEY: CDS | | | | | | | | |
| ; | LOCATION: 56..3454 | | | | | | | | |
| ; | OTHER INFORMATION: /product= "hprt" | | | | | | | | |
| ; | /note= "human telomerase reverse | | | | | | | | |
| ; | transcriptase (hprt) catalytic protein | | | | | | | | |
| ; | component" | | | | | | | | |
| ; | SEQUENCE DESCRIPTION: SEQ ID NO: 224: | | | | | | | | |
| ; | US-10-054-295-224 | | | | | | | | |
| | Query Match | 100.0%; | Score | 901; | DB | 14; | Length | 4015; | |
| | Best Local Similarity | 100.0%; | Pred. | No. 6.6e-242; | | | | | |
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| DB | 1969 | CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCGGAGCGTCTCACTCGAGGGT | 2028 | | | | | | |
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| QY | 181 | CTCTGTGCTGGGCGCTGGACGATATCCACAGGGCGCTGGCGCACTTCGTGTGTGGTGTGCG | 240 | | | | | | |
| DB | 2089 | CTCTGTGCTGGGCGCTGGACGATATCCACAGGGCGCTGGCGCACTTCGTGTGTGGTGTGCG | 2148 | | | | | | |
| QY | 241 | GGCCAGAGCCCGCGCTCAGCTGATGTTGTCAAGTGTGATGTGACGGCGCGTACGA | 300 | | | | | | |
| DB | 2149 | GGCCAGAGCCCGCGCGCTCAGCTGATGTTGTCAAGTGTGATGTGACGGCGCGTACGA | 2208 | | | | | | |
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| DB | 2209 | CACCATCCCCAGSACAGAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAC | 2268 | | | | | | |
| QY | 361 | GTACTGGTGGTGGTATCGGTGTHCCAGAGCGGCCCATGTGGGCACATCCGCAAGGC | 420 | | | | | | |
| DB | 2269 | GTACTGGTGGTGGTATCGGTGTHCCAGAGCGGCCCATGTGGGCACATCCGCAAGGC | 2328 | | | | | | |
| QY | 421 | CTTCAAGAGCCAGTCTCTACCTTGACAGACCTCCAGCCCTACATGGACAGTTCGTGGC | 480 | | | | | | |
| DB | 2329 | CTTCAAGAGCCAGTCTCTACCTTGACAGACCTCCAGCCCTACATGGACAGTTCGTGGC | 2388 | | | | | | |
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| DB | 2389 | TCACCTGCAGGAGACCAAGCCCGGTGAGGGATGCGGTCTCATCGAGCAGAGCTCCTCCCT | 2448 | | | | | | |
| QY | 541 | GAATGAGGCCAGAGTGGCCTCTTTCGACGCTTTCCTTACGTTTCATGTGCGCACACGCCGT | 600 | | | | | | |
| DB | 2449 | GAATGAGGCCAGAGTGGCCTCTTTCGACGCTTTCCTACGTTTCATGTGCGCACACGCCGT | 2508 | | | | | | |
| QY | 601 | CGGCATCAGGGGCAAGTTCCTACGTCCAGTGGCAGGGGATCCCGCAGGGCTCCATCCTCTC | 660 | | | | | | |
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| DB | 2569 | CAGCTGCTCTGCAGCCTGTGCTACGCGACATGGAGAAAGAGTGTTTCGGGGGATTCG | 2628 | | | | | | |
| QY | 721 | CGCGGAGCGGCGTGTCTCTCGCGTTTGTGTGGATGATTTTCTTGTGTGACACCTCACCTCAC | 780 | | | | | | |

Db 2629 GCGGGAGGGCTGCTCTGGGTTGGGATGATTTCTTGTGGTACACCTCACCTCAC 2688
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QY 841 GAACCTCGGGAAGACAGTGTGTAACCTTCCCTGTAGAAAGACGAGCCCTGGGTGGCAGCGC 900
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Db 2809 T 2809

RESULT 12

US-10-054-611-224
; Sequence 224, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
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; OTHER INFORMATION: /product= "hprt"

; /note= "human telomerase reverse
; transcriptase (hprt) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-611-224
Query Match 100.0%; Score 901; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCAGACTCGGCTTCATCCCAAGCCTGACGGGCTGGGCCGATGTGTAACATGAGACTA 60
Db 1909 GTCCAGACTCGGCTTCATCCCAAGCCTGACGGGCTGGGCCGATGTGTAACATGAGACTA 1968
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Db 2089 CTCTGTCTGGGCTTGGACGATATCCACAGGGCTTGGGCGACCTTCGTGTCGTGTGCG 2148
QY 241 GGGCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGCGGTACGA 300
Db 2149 GGGCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGCGGTACGA 2208
QY 301 CACCATCCCCAGGACAGGCTCACGAGGTATCCGCCAGCATATCAAAACCCAGAACAC 360
Db 2209 CACCATCCCCAGGACAGGCTCACGAGGTATCCGCCAGCATATCAAAACCCAGAACAC 2268
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Db 2269 GTACTGCTGCGTGGTATGCCGTGGTCCAGAAAGCGCCCGTGGGCGACGTCGCCAAGGC 2328
QY 421 CTTCAAGAGCCACGCTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGC 480
Db 2329 CTTCAAGAGCCACGCTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGC 2388
QY 481 TCACCTGCAGAGACACAGCCCGCTGAGGGATGCGCTCATCAGCAGAGCTCCTCCCT 540
Db 2389 TCACCTGCAGAGACACAGCCCGCTGAGGGATGCGCTCATCAGCAGAGCTCCTCCCT 2448
QY 541 GAATGAGCCAGCAGTGGCCTCTTCGACGCTTCCTTACGCTTCATGTGCCACACGCGCT 600
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QY 841 GAACCTCGGGAAGACAGTGTGTAACCTTCCCTGTAGAAAGACGAGCCCTGGGTGGCAGCGC 900
Db 2749 GAACCTCGGGAAGACAGTGTGTAACCTTCCCTGTAGAAAGACGAGCCCTGGGTGGCAGCGC 2808
QY 901 T 901
Db 2809 T 2809

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US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR FILING DATE: 2002-03-21
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
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; LOCATION: (56)...(3454)
; OTHER INFORMATION:
US-10-105-963-1

Query Match 100.0%; Score 901; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

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;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002600US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 576-0200
;     TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 1:
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;       LENGTH: 4015 base pairs
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Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CGTGTGGGAGCAGAGAGCTTCGACAGAAAGAGGGCGGAGGCTCACCTCGAGGGT 120
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QY 241 GGCCAGAGCCCGCGCTGAGTGTACTTTGCAAGGTGATGTGACGGCGGTACGA 300
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; Publication No. US2003010093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin
;             Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;                   THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 11-Jan-2002
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
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; APPLICATION NUMBER: US 08/854,050
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; APPLICATION NUMBER: US 08/851,843
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; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
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; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
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TOPOLOGY: linear
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Best Local Similarity 100.08; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Marin, Gregg B.
; APPLICANT: Haxley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851-843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
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 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002930US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 224:
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| ; | FILING DATE: | 18-APR-1997 |
| ; | CLASSIFICATION: | |
| ; | PRIOR APPLICATION DATA: | |
| ; | APPLICATION NUMBER: | US 08/724,643 |
| ; | FILING DATE: | 01-OCT-1996 |
| ; | CLASSIFICATION: | |
| ; | ATTORNEY/AGENT INFORMATION: | |
| ; | NAME: | Apple, Randolph T. |
| ; | REGISTRATION NUMBER: | 36,429 |
| ; | REFERENCE/DOCKET NUMBER: | 015389-002930US |
| ; | TELECOMMUNICATION INFORMATION: | |
| ; | TELEPHONE: | (415) 576-0200 |
| ; | TELEFAX: | (415) 576-0300 |
| ; | INFORMATION FOR SEQ ID NO: | 224: |
| ; | SEQUENCE CHARACTERISTICS: | |
| ; | LENGTH: | 4015 base pairs |
| ; | TYPE: | nucleic acid |
| ; | STRANDEDNESS: | single |
| ; | TOPOLOGY: | linear |
| ; | MOLECULE TYPE: | cdna |
| ; | FEATURE: | |
| ; | NAME/KEY: | CDS |
| ; | LOCATION: | 56..3454 |
| ; | OTHER INFORMATION: | /product= "htrt" |
| ; | OTHER INFORMATION: | /note= "human telomerase reverse |
| ; | OTHER INFORMATION: | transcriptase (hTERT) catalytic protein |
| ; | OTHER INFORMATION: | component" |
| ; | US-08-851-843A-224 | |
| Alignment Scores: | | |
| Pred. No.: | 0 | Length: 4015 |
| Score: | 6057.00 | Matches: 1150 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 99.64% | Indels: 0 |
| DB: | 3 | Gaps: 0 |
| US-08-951-733-20 (1-1154) x US-08-851-843A-224 (1-4015) | | |
| QY | 5 | GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24 |
| Db | 2 | CAGCGCTGGTCTCTGCTGGCAGCTGGGAAGCCCTGGCCCGCCACCCCGCGATGCCG 61 |
| QY | 25 | ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44 |
| Db | 62 | CGCGTCCCGCTGCCGAGCGGTGGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTG 121 |
| QY | 45 | ProLeuAlaThrPheValArgLeuGlyProGlnGlyTyrArgLeuValGlnArgGly 64 |
| Db | 122 | CCGCTGGCCACGTTTCGTGGCGCGCTGGGGCGCCAGAGGCTGGCGGCTGGTGCAGCGCGG 181 |
| QY | 65 | AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84 |
| Db | 182 | GACCGCGGCTTTCGCGCGCTGGTGGCCAGTGCCTGTGTGCTGGTGGCTGGGACGCA 241 |
| QY | 85 | ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104 |
| Db | 242 | CGCGCGCGCGCGCGCGCGCTCTCTCCCGCAGGTGCTCCTGCCTGAAGAGCTGGTGGCC 301 |
| QY | 105 | ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124 |
| Db | 302 | CGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTCGTGGCTTCGGCTTCGCG 361 |
| QY | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144 |
| Db | 362 | CTGCTGGACGGGCGCGCGGGGCGCGCGCGCTTACACCGAGGCTTACACCGCGTGCAGCTAC 421 |
| QY | 145 | LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164 |
| Db | 422 | CTGCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCTGGTGGGCTGCTGCTGCGC 481 |
| QY | 165 | ArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184 |

| | | | |
|----|------|---|------|
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla | 564 |
| DB | 1622 | AGCCAGGGGTGGCTGTGTCCGGCCGACAGCACCGTCTGGGTGAGGAGATCTGGCC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr | 584 |
| DB | 1682 | AAGTTCCTGCACCTGGCTGATGAGTGTGCTGCTCGAGCTGCTCAGGCTCTTTTAT | 1741 |
| QY | 585 | ValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| DB | 1742 | GTCACGGAGCACCGTTTCAAAGAACACAGCTCTTTTCTACCGGAAGAGTGTCTGGAGC | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 |
| DB | 1802 | AAGTTGCAAGCATTTGGAATCAGACACGACTTGAAGAGGTGCGAGTCCGGGAGCTGTCG | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| DB | 1862 | GAACGAGGTCAGCGACGATCGGGAGCAGGCCCGCCCTGCTGAGCTCCACACTCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| DB | 1922 | TTTCATCCCCAAGCCTGACGGGCTCGGCCCATTTGTAACATGGACTACGTCGTGGGAGCC | 1981 |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| DB | 1982 | AGAACGTTCCGACAGAAAAAGAGGGCCGCGCTCTACCTCGAGGTTGAAGGCACCTGTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
| DB | 2042 | AGCGTGTCAACTACGAGCGGGCGCGCCCGGCTCTCGGGCGCTCTGCTGTGGGC | 2101 |
| QY | 705 | LeuAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 |
| DB | 2102 | CTGCACGATATCCACAGGGCTGCGGCACCTGCTGCTGCTGGGGCCACGAGACCCG | 2161 |
| QY | 725 | ProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 |
| DB | 2162 | CCGCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACCATCCCCAG | 2221 |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 |
| DB | 2222 | GACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACAGTACTCGTGGGT | 2281 |
| QY | 765 | ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
| DB | 2282 | CGGTATCCCTGGTGTCCAGAAGCGGCCCATGGCACGTCGCGAAGGCTTCAAGAGCCAC | 2341 |
| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 |
| DB | 2342 | GTCTCTACCTTGACAGACCTCCAGCCGTACATCGGACAGTTCTGGCTCACTTGCAGGAG | 2401 |
| QY | 805 | ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 |
| DB | 2402 | ACCAGCCCGTGAAGGATGCGCTCGTCATCGACGAGAGCTCCCTCCCTGAATGAGGCCAGC | 2461 |
| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly | 844 |
| DB | 2462 | AGTGGCCCTTCGACGCTTTCCTACGCTTCATGTGCCACCCACGCCCTGGCGCATCAGGGC | 2521 |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| DB | 2522 | AAGTCTTACGTCAGTGCCAGGGGATCCCGAGGGGTCCATCTCTCCAGCTGTCTGTGC | 2581 |
| QY | 865 | SerLeuCystTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgaspGlyLeu | 884 |
| DB | 2582 | AGCCTGTGCTCAGCGACATGGAGAACAAAGCTCTTTGGGGGATTCGCGGGACGGGCTG | 2641 |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHisAlaLysThr | 904 |
| DB | 2642 | CTCCTGGTGTGGTGAATGATTTCTGTGGTGACACCTCACCTCACCCACCGGAAAC | 2701 |

| | | | |
|----|------|---|------|
| Qy | 905 | PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 |
| Db | 2702 | TTCTCTCAGGACCCCTGGCTCCGAGGTGTCCTCTAGTATGGCTGCCTGGTGAACCTTGC | 2761 |
| Qy | 925 | ThrValValAsnPheProValGluAspGluAlaLeuGlyThrAlaPheValGlnMet | 944 |
| Db | 2762 | ACAGTGGTGAACCTTCCCTGTGTAGAAGACGAGCCCTGGGTGGCGACGGCTTTGTTCAGATG | 2821 |
| Qy | 945 | ProAlaHisGlyLeuPheProTyrCpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal | 964 |
| Db | 2822 | CCGCGCCACGSGCCATTCCCTGTGTGGCCCTGCTGTGGATACCCGGACCCCTGGAGGTG | 2881 |
| Qy | 965 | GlnSerAspTyrSerSerTyrAlaAArgThrSerIleArgAlaSerLeuThrPheAsnArg | 984 |
| Db | 2882 | CAGAGCGACTACTCTCAGCTATGCCCGGACCTCCATCATCAGAGCCAGTCTCACTTCAACCGC | 2941 |
| Qy | 985 | GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys | 1004 |
| Db | 2942 | GGCTTCAAGGCTGGAGAGACATCGCTCGCAACATCTTTGGGTGCTTTCGGCTGAAGTGT | 3001 |
| Qy | 1005 | HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr | 1024 |
| Db | 3002 | CACAGCCTGTTTCTGGATTTCAGGTGAACAGCCCTCCAGAGGTGTGCACCAACATCTAC | 3061 |
| Qy | 1025 | LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis | 1044 |
| Db | 3062 | AAGATCTCTCTGCTGCAGGCGTACAGTTCACGCATGTGTGCTGCAGCTCCCATTTTCAT | 3121 |
| Qy | 1045 | GlnGlnValTrpLysAsnProThrPheLeuArgValIleSerAspThrAlaSerLeu | 1064 |
| Db | 3122 | CAGCAAGTTTGGAAAGACCCACATTTTCTCGCGCTCATCTCTGACAGCGCTCCCTC | 3181 |
| Qy | 1065 | CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla | 1084 |
| Db | 3182 | TGCTACTCCATCTCTGAAAGCCAGAACGCGAGGATGTCTGCTGGGGGCCAAGGCGCGCC | 3241 |
| Qy | 1085 | GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLysLeu | 1104 |
| Db | 3242 | GGCCCTCTGGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTCAAGCTG | 3301 |
| Qy | 1105 | ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln | 1124 |
| Db | 3302 | ACTCGACACCGTGTACCTAGTGTCCACTCTTGGGGTCACTCTCAGGACAGCCGACGACG | 3361 |
| Qy | 1125 | LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaLysAsnProAla | 1144 |
| Db | 3362 | CTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCGCTTGGGCGCGCGACCAACCCGCGCA | 3421 |
| Qy | 1145 | LeuProSerAspPheLysThrIleLeuAsp | 1154 |
| Db | 3422 | CTGCCCCACACTTCAAGACCATCTCTGGAC | 3451 |

RESULT 2

US-08-974-549A-1
: Sequence 1, Application US/08974549A
: Patent No. 6166178
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: APPLICANT: Lingner, Joachim
: APPLICANT: Nakamura, Toru
: APPLICANT: Chapman, Karen B.
: APPLICANT: Morin, Gregg B.
: APPLICANT: Harley, Calvin B.
: APPLICANT: Andrews, William H.
: TITLE OF INVENTION: Human Telomerase Catalytic Subunit
: NUMBER OF SEQUENCES: 727
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "htrr"
OTHER INFORMATION: /note= "human telomerase reverse
OTHER INFORMATION: transcriptase (htrr) catalytic protein
US-08-974-549A-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 3 Gaps: 0

US-08-951-733-20 (1-1154) x US-08-974-549A-1 (1-4015)

QY

5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24

| | | | |
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| Db | 2 | CAGCGCTCGCTCTCGTCGACGCTGGGAAGCCCTGGCCCGCCGACCCCGCGATGCGG | 61 |
| QY | 25 | ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlnValLeu | 44 |
| Db | 62 | CGCGCTCCCGCTGCCGAGCGTGCCTCCCTGCTGCCGACCACTACCGGAGGTGCTG | 121 |
| QY | 45 | ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly | 64 |
| Db | 122 | CGCTGGCCACGTTCTGTCGCGCCCTGGGCCCCCAGGGCTGGCGGCTGGTGGACGGG | 181 |
| QY | 65 | AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla | 84 |
| Db | 182 | GACCGCGCGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGGCTGCCCTGGACGCA | 241 |
| QY | 85 | ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla | 104 |
| Db | 242 | CGCGCGCCCCCGCGCCCTCTCTCCGCGAGGTGCTGCTGAAGAGGTGGTGCC | 301 |
| QY | 105 | ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla | 124 |
| Db | 302 | CGAGTGTGCAGAGGCTGTGCGAGCGCGCGAAGACGTGCTGGCCTTCGGCTTCGGG | 361 |
| QY | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr | 144 |
| Db | 362 | CTGCTGGACGGGCGCGGGGCGCCCGAGGCTTACCCAGCGCTGCGCAGCTAC | 421 |
| QY | 145 | LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg | 164 |
| Db | 422 | CTGCCAACACGGTGACGACGACTGCGGGGAGCGGGGCTGGGGGCTGCTGCTGGCC | 481 |
| QY | 165 | ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal | 184 |
| Db | 482 | CGCGTGGCGACGACGCTGCTGTTCACTGTGGCAGCTGCGCGCTCTTTGTGCTGGT | 541 |
| QY | 185 | AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr | 204 |
| Db | 542 | GCTCCACGCTGGCTACCGAGGTGTGGGGCGCGGCTGTACCACTGCGGCGCTGCCACT | 601 |
| QY | 205 | GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla | 224 |
| Db | 602 | CAGCGCGCGCGCGCCACGCTAGTGGACCCCGAAGCGCTGCGGATGCGAAGCGGCC | 661 |
| QY | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| Db | 662 | TGGAACCATAGCTCAGGAGCGGGGTCCCGCTGGGCTGCCAGCCCGCGGTGCGAGG | 721 |
| QY | 245 | ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla | 264 |
| Db | 722 | AGCGCGGGGCGAGTGCAGCCGAACTGCTGCGTGGCCCAAGAGCGCCCGCGCTGCT | 781 |
| QY | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| Db | 782 | CCCCCTGAGCCGGAGCGGACCGCCGTTGGGCGAGGGTCTGGGCCCCCGCGGAGGACG | 841 |
| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| Db | 842 | CGTGGACGAGTACCGGTGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 901 |
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| Db | 902 | ACCTCTTTGGAGGGTGCCTCTCTGCGACGCGGCACTCCCACTCCATCCATCCATCCAT | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| Db | 962 | CACCACGG | 1021 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| Db | 1022 | CCGGTGTACCGCGAGACCAACCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCT | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |

| | | | |
|----|------|---|------|
| Db | 1082 | CCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCGCTGACTGGCGCTCGGAGGCTCTGGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| Db | 1142 | ACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTGGCCCGCCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCCAGCGTACTGGCAATATGCGGCCCTGTCTTGAGCTGCTTGGGAACACAGCGCAG | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTCGAGCTCGGGTCACCCCAGCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| Db | 1322 | GCCGGTGTCTGCCCGGGAGAACCCCAAGGCTCTGTGGCGCCCGCCAGAGAGGAGAC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| Db | 1382 | ACAGACCCCGTGCCTGGTGCAGCTGCTCCGCCACACAGCAGCCCTGGCAGGTGTAC | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| Db | 1442 | GGCTTCGTGGGCGCTGCCTGCGCGGCTGGTCCCGCCAGGCCCTCGGGCTCCAGGCAC | 1501 |
| QY | 505 | AsnGluArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 |
| Db | 1502 | AAGAAACGGCGCTTCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAAGCATGCCAAG | 1561 |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArg | 544 |
| Db | 1562 | CTCTCGCTGAGGAGCTGAGTGGGAAGATGAGGTGCGGAGCTGCGCTTGGCTGGCGAGG | 1621 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla | 564 |
| Db | 1622 | AGCCAGGGGTTGGCTGTGTTCCGGCGCGAGACACCGCTCGCTGAGGAGATCCTGGCC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr | 584 |
| Db | 1682 | AGTTCTCTGCACGTGGTGTAGTGTGTACGTCTCGAGCTGCTCAGGTCTTTCTTTAT | 1741 |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| Db | 1742 | GTCACGGAGACCACTTTCNAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGAGC | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 |
| Db | 1802 | AAGTTCAAAGCATTGGAAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGCG | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| Db | 1862 | GAAGCAGAGGTCAAGGAGCATCGGAAGCCAGCGCCGCTGCTGACGTCCAGACTCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| Db | 1922 | TTATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGAGCC | 1981 |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| Db | 1982 | AGAACGTTCCGCAGAGAAAGAGCGCGAGCGTCTCACCTCAGGGGTGAAGGCACGTTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
| Db | 2042 | AGCGTGTCAACTACGAGCGGCGCGCGCCCGCTCTCTGGCGCTCTGTGTGGGC | 2101 |
| QY | 705 | LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 |
| Db | 2102 | CTGGAGATATCCACAGGCGCTGGCGACCTTCGTGCTGGGTGGCGCCAGGACCCG | 2161 |
| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 |
| Db | 2162 | CCGCTTGAGCTGTACTTTGTCAAGTGGATGTACCGGGCGGTACACACCATCCCCAG | 2221 |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 |
| Db | 2222 | GACAGGCTCAGCGAGGTCTATCGCCAGCATCAAAACCCAGAACACGTACTCGTCGT | 2281 |
| QY | 765 | ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
| Db | 2282 | CGGTATGCGGTGTCCAGAAGCGCCCATGGCAGCTCCGCAAGGCTTCAAGAGCCAC | 2341 |
| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 |
| Db | 2342 | GTCTCTACCTTGACAGACCTCCAGCGTACATCGCAGTTCTGTGGCTCACCTGCAGGAG | 2401 |
| QY | 805 | ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 |
| Db | 2402 | ACCAGCCCGGTGAGGATGCCGTGTCATCGCAGCAGCTCCCTCGTAATGAGGCCAGC | 2461 |
| QY | 825 | SerGlyLeuPheAspValPheLeuLeuArgPheMetCysHisAlaValArgIleArgGly | 844 |
| Db | 2462 | AGTGGCTCTTTCGACGTCTTCCCTACCGTTCGTGCCACCACCGCGGTGCCATCAGGGG | 2521 |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| Db | 2522 | AAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGCG | 2581 |
| QY | 865 | SerLeuCystTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 |
| Db | 2582 | AGCTGTGCTACGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCTG | 2641 |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr | 904 |
| Db | 2642 | CTCTCGCTTGTGGTGTATTTCTTGTGTGACACCTCACCTCACCCAGCGGAAACCC | 2701 |
| QY | 905 | PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 |
| Db | 2702 | TTCTCAGGACCTGTGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTGGCGAG | 2761 |
| QY | 925 | ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet | 944 |
| Db | 2762 | ACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGCACGGCTTTGTTCAGATG | 2821 |
| QY | 945 | ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal | 964 |
| Db | 2822 | CCGGCCCCAGCCCTATTCCTCGTGGCGGCTGCTGCTGTATACCGGAGCCCTGGAGGTG | 2881 |
| QY | 965 | GlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg | 984 |
| Db | 2882 | CAGAGCGACTACTCCAGCTATGCCGAGACCTCCATCAGAGCCAGTCTCACCTTCAACCGC | 2941 |
| QY | 985 | GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys | 1004 |
| Db | 2942 | GGCTTCAAGGCTGGGAGAACATGCGCTGCNAACCTCTTTGGGCTCTTGGCGCTGAAGTG | 3001 |
| QY | 1005 | HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr | 1024 |
| Db | 3002 | CACAGCTGTCTTGTGATTTGCAGGTGAACAGGCTCCAGAGGTGTGTGCACACATCTAC | 3061 |
| QY | 1025 | LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis | 1044 |
| Db | 3062 | AAGATCTCTCTGTCAGGCGTACAGGTTTTCAGCATGTGTGTGTGCAGCTCCCATTTTCAT | 3121 |
| QY | 1045 | GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu | 1064 |
| Db | 3122 | CAGCAAGTTTGGAAAGAACCCACATTTTCTCGCGCTCATCTCTGTACAGGGCTCCCTC | 3181 |
| QY | 1065 | CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla | 1084 |
| Db | 3182 | TGCTACTCTCTGAAAGCCAAAGACGAGGATGTGCTGGGGGCCAAAGGGCGCGGCC | 3241 |
| QY | 1085 | GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu | 1104 |
| Db | 3242 | GGCCCTCTGCGCTCCGAGGCGGTGCAGTGGCTGTGCCCAAGCATTCCTGCTCAAGCTG | 3301 |

QY 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
Db 3302 ACTGACACCGGTGTACCTAGTGCCTCTGGGGTCACTCAGGACAGCCAGCGAG 3361
QY 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
Db 3362 CTGAGTCGGAAGCTCCCGGGGACGACGTGACTGCCCTGGAGCGCGCAACCCGCGCA 3421

QY 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
Db 3422 CTGCCCTCAGACTTCAGACCATCTCGAC 3451

RESULT 3

US-08-854-050-224
; Sequence 224, Application US/08854050
; Patent No. 6261836

GENERAL INFORMATION:

APPLICANT: Tech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO.6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854.050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/951.843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846.017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844.419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724.643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

; NAME/KEY: CDS
; LOCATION: 56...3454
; OTHER INFORMATION: /product= "hrrt"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hrrt) catalytic protein
; OTHER INFORMATION: component"
US-08-854-050-224

Alignment Scores:

Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 3 Gaps: 0

US-08-951-733-20 (1-1154) x US-08-854-050-224 (1-4015)

QY 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
Db 2 CAGCGCTGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCGCCACCCCGCGATGCG 61
QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTGCCGAGCGGTGGCTCCCTGGTGGCAGCCACTACCGGAGGTGCTG 121
QY 45 ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGTGGCCACGTTGCTGGCGGCGCTGGGGGCCCGCAGGCGCTGGGCTGGTGGCGCGG 181
QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCGCGCGCTTCCGCGCGCTGGTGGCCCGCTGGTGGTGGTGGTGGTGGTGGTGG 241
QY 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCGCGCGCGCGCGCGCTCTCCGCGCAGGTGTCTGCTGCTGAGGAGTGGTGCC 301
QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTGCAGAGGTGTGGAGCGCGCGCGGAGACGTGTGGCTTGGCTTGGCTTGG 361
QY 125 LeuLeuAspGlyAlaArgGlyGlyProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGGAGCGGCGCGCGCGCGCGCGCTTCCACCGAGGCTTCCACCGAGCGTGGCAGCTAC 421
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
Db 422 CTGCCCAACCGGTGACCGCGCTGGCGGGGAGCGGGGCGTGGGCGTGGTGGTGGTGG 481
QY 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
Db 482 CGCGTGGCGGACGAGCTGCTGGTTCACCTGTGGCAGCGCTGGGCGCTCTTTGTGCTGGTG 541
QY 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGGCTACCGAGTGTGGCGCGCGCGCTGTACAGCTGGCGCTGGCGCTGGCCT 601
QY 205 GlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
Db 602 CAGGCGCGCGCGCGCGCGCGCTAGTGGACCGCGCGCGCGCTGGGATGGGAACGGGCC 661
QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
Db 662 TGGAACCATAGCTCAGGAGCGCGGGTCCCGCTGGGCTTGCAGCGCGCGCGGTTGGAGG 721
QY 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264
Db 722 AGCGCGGGGGCAGTGGCCAGCCGAAGTCTGCGGTGGCCAAAGAGGCGCCAGCGCTGGCGCT 781
QY 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
Db 782 GCCCTTGAGCGGAGCGGACCGCGCTGGGCGAGGGGTCTCTGGGCGCCACCGCGGCGAGGACG 841

Db 3002 CACAGCCTGTTCTGGATTGTCAGGTGAACAGCCTCCAGAGGTGTGCACCAACATCTAC 3061
Qy 1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
Db 3062 AAGATCCTCTGCTGCAGGGGTACAGGTTTCACGCATGTGTGTGCAGCTCCCATTTTCAT 3121
Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
Db 3122 CAGCAAGTTTGGAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCCTC 3181
Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaClyMetSerLeuGlyAlaLysGlyAlaAla 1084
Db 3182 TGTACTCCATCTCTGAAAGCAAGACGAGGGATGTCGTGGGGGCCAAGGGCGCGCC 3241
Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
Db 3242 GGCCCTCTGCCCTCCGAGGGCGTGCAGTGGCTGTGCCACCAAGCATTTCTGTCAAGCTG 3301
Qy 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
Db 3302 ACTGCACAGCTGTACACTAGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGACGACG 3361
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
Db 3362 CTGAGTCGGAAGCTCCCGGGGAGCAGCTGACTGCCCTGGAGGCGCGCAACCCGGCA 3421
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
Db 3422 CTGCCCTCAGACTCAGACCATCTCTGGAC 3451

RESULT 4

US-09-430-323-224
: Sequence 224, Application US/09430323
: Patent No. 6309867
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: Lingner, Joachim
: Nakamura, Toru
: Chapman, Karen B.
: Morin, Gregg B.
: Harley, Calvin
: Andrews, William H.
: TITLE OF INVENTION: No. 6309867el Telomerase
: NUMBER OF SEQUENCES: 225
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: FILING DATE: 09/09/430,323
: FILING DATE: 29-Oct-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/854,050
: FILING DATE: 09-MAY-1997
: APPLICATION NUMBER: US 08/851,843
: FILING DATE: 06-MAY-1997
: APPLICATION NUMBER: US 08/846,017
: FILING DATE: 25-APR-1997
: APPLICATION NUMBER: US 08/844,419
: FILING DATE: 18-APR-1997
: APPLICATION NUMBER: US 08/724,643
: FILING DATE: 01-OCT-1996
: ATTORNEY/AGENT INFORMATION:

: NAME: Apple, Randolph T.
: REGISTRATION NUMBER: 36,429
: REFERENCE/DOCKET NUMBER: 015389-002930US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 224:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4015 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cdna
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 56..3454
: OTHER INFORMATION: /product= "hTERT"
: /note= "human telomerase reverse
: transcriptase (hTERT) catalytic protein
: component"
: SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-430-323-224

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 4 Gaps: 0

US-08-951-733-20 (1-1154) x US-09-430-323-224 (1-4015)

Qy 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
Db 2 CAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCGCACCCCGCGATGCCG 61
Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTGCTCGGAGCGCTGCGCTCCCTGCTGCGACGCCACTACCGGAGGTGCTG 121
Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGCTGGCCACGTTTCGTGCGCGCTGCGGCCCGCCAGGCGCTGGCGCTGGTGCACGCGGG 181
Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCCGGCGCTTCCCGCGCTGCTGGCCAGTGCCTGGTGTGCTGCGCTGGGACGCA 241
Qy 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCCCGCGCGCCCTCTCTCCGCCAGGTGCTCCTGCTGAAGAGGTGTTGGCC 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTGCAGAGCTGTGCGAGCGGCGGCGAAGAACGTCGTGCGCTTCGGCTTCGCG 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGACGGGGCGCGGGGGCCCCCGAGGCCCTTCACCCAGCGTGCAGGTAC 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrPglyLeuLeuArg 164
Db 422 CTGCCCAACACGGTGACCGACCTCGGGGGAGCGGGCGTGGGGGCTGCTGCTGCGC 481
Qy 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
Db 482 CGCGTGGCGACGACGTCGTGTTTACCTGTGTCACGCTGTCGACGCTCGCGGCTCTTTGTGCTGTG 541
Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGCGCCTACCGAGGTGTGGGGGGCGCGCTGTACCGAGCTCGGCGCTGCCACT 601

| | | | |
|----|------|--|------|
| QY | 205 | GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla | 224 |
| Db | 602 | CAGGCCGCCGCCGCCACACCTAGTGGAGCCCGAGGCGTCTGGATGCGAAGCGCC | 661 |
| QY | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| Db | 662 | TGGAACCATAGCGTCAGGAGGCGCGGTCCCGCTGGCGCTGCCAGCCCGCGGTGCGAGG | 721 |
| QY | 245 | ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla | 264 |
| Db | 722 | AGGCGCGGGCGAGTGCAGCGCGAAGTCTGCCGTTCGCCAAGAGGCCCGCGGTGCGCGT | 781 |
| QY | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGlyArgThr | 284 |
| Db | 782 | GCCTCTGAGCCGAGCGGAGCGCCGTTGGCGAGGGTCTTGGGCCACCCCGGCGAGGAGC | 841 |
| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| Db | 842 | CGTGACCGAGTGCAGCGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 901 |
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| Db | 902 | ACCTCTTTGGAGGGTGCCTCTCTGTCAGCGGCCACTCCACCATCCGTGGGGCGCCAG | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrProCysPro | 344 |
| Db | 962 | CACACGCGGGGCCCGCCATCCACATCGCGGCCACACACGTCCTCGGACGCGCTGTGCC | 1021 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| Db | 1022 | CGGGTGTACGGCGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAAGAGCAGCTGCGG | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| Db | 1082 | CCCTCTCTCTACTCAGCTCTCTGAGGCCCGCCCTGACTGGCGCTCGGAGGCTCGTGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| Db | 1142 | ACCATCTTCTGGGTTCAGGCCCTCGATGCGCAGGAGCTCCCGCAGGTGTCGCCGCGCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCCAGCGCTACTGCATAATGGCGGCCCTGTCTCTGGAGCTGCTGGGAACACACGCGCAG | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCTACGGGGTGTCTCTAAGACGCACTCCCGCTGCGAGCTGCGGCTCACCCGACCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| Db | 1322 | GCCGTTGTGTGCCCCGGAGAACGCCCGAGGGCTCTGTGGCGGCCCGCCGAGGAGGAGAC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| Db | 1382 | ACAGACCCCGCTGCTGGTGGAGCTGTCTCCCGCAGCACAGCAGCCCTGGCAGGTGTAC | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| Db | 1442 | GGCTTCGTGCGGGCTGCTGCGCGGGTGTGTGCGCCCGCCAGGCTCTGCGGCTCCAGGCAC | 1501 |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 |
| Db | 1502 | AACGAACCGCGTCTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAAG | 1561 |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 |
| Db | 1562 | CTCTCGCTGCAGAGCTGACGTGGAAGATGACCGTGGCGGGACTGCGCTTGGCTGGCAGG | 1621 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluLeuLeuAla | 564 |
| Db | 1622 | AGCCCGAGGGTGTGTGTCTCCGCGCCGAGAGCACCGTCTCGGTGAGGAGATCCTGGCC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr | 584 |
| Db | 1682 | AAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCTGCGAGCTCTCAGGTCTTTCTTTAT | 1741 |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| Db | 1742 | GTACGGAGACACCGTTCAAAAGAACAAGCGTCTTTTCTACCGGAAGAGTGTCTGGAGC | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValClnLeuArgGluLeuSer | 624 |
| Db | 1802 | AAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGAGCTGTGC | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| Db | 1862 | GAAACAGAGTTCAGCAGCATCGGNAAGCAGCCCGCCCTGCTGACGTCCAGACTCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| Db | 1922 | TTTCATCCCAAGCCTGACGGCTGCGCGGATTTGAACATGGACTACGTCTGTTGGAGCC | 1981 |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| Db | 1982 | AGAAGCTTCGCGAGAGAAAGAGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACGTTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuGlyAlaSerValLeuGly | 704 |
| Db | 2042 | AGCGTGTCACTACGAGCGCGCGCGCCCGCGCTCTGGCGCCCTCTGTGCTGGGC | 2101 |
| QY | 705 | LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 |
| Db | 2102 | CTGGACGATATCCACAGGCGCTGGCGACCTCTGCTGCTGCTGCTGCGGCCAGGACCG | 2161 |
| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 |
| Db | 2162 | CGCGCTGAGCTGTACTTGTCAAGTGGATGTGACGGCGGTGACACACCATCCCGCCAG | 2221 |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 |
| Db | 2222 | GACAGGCTCACGGAGTCTATCGCCAGCATCATCAACCCAGACACGTACTGCTGCGT | 2281 |
| QY | 765 | ArgTyrAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
| Db | 2282 | CGGTATGCGTGTCTCAGAAGCGCGCCATGGCAGCTCGCAAGCGCTTCAAGAGCCAC | 2341 |
| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 |
| Db | 2342 | GTCTTACCTTACAGACCTCCAGCGTATCATGCGACATTCGTGCTCACCCTGACGAG | 2401 |
| QY | 805 | ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 |
| Db | 2402 | ACCAGCCCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCTCTGATGAGGCCAGC | 2461 |
| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly | 844 |
| Db | 2462 | ACTGGCTCTTCGACGTCTTCTACGCTTCATGTGCGCACACCGCCCTGGCATCAGGGC | 2521 |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| Db | 2522 | AAGTCTACGTACGTCCAGGGGATCCGCGAGGCTCCATCTCTCCACGCTGCTGCTGC | 2581 |
| QY | 865 | SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 |
| Db | 2582 | AGCCGTGTCTCGGCGACATGGAGAACAAAGCTGTTTTCGGGGATTCGGCGGAGCGGCTG | 2641 |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr | 904 |
| Db | 2642 | CTCCTCGCTTGGTGGATCATTTCTTGTGTTGGTGGACACCTCACCTCACCGCGAACC | 2701 |
| QY | 905 | PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 |
| Db | 2702 | TTCTCTCAGGACCTGCTGCGAGGTGCTGCTGAGTATGGTGGTGGTGAATTCGCGAAG | 2761 |
| QY | 925 | ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet | 944 |

Db 2762 ACAGTGGTGAACCTCCCTGTAGAACGACGAGGCCCTGGGTGGCAGCGGCTTTGTTCAGATG 2821
Qy 945 ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuVal 964
Db 2822 CCGGCCACAGCGCTATTCCCTGGTGGGCTGTCTGGATACCCGAGACCTGGAGTG 2881
Qy 965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984
Db 2882 CAGAGCGACTACTCCAGCTATGCGCGAGCCTCCATCATCAGAGCCAGTCTCACTTCAACCGC 2941
Qy 985 GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004
Db 2942 GGCTTCAAGCGCTGGGAGACATCGTCGCAACTCTTTGGGCTTTGGCGCTGAAGTGT 3001
Qy 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
Db 3002 CACAGCCTGTTCTGGATTGTCAGGTGAACAGCCTCCAGAGGTGTGCACCAACATCTAC 3061
Qy 1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
Db 3062 AAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCAATGTGTGTGCAGCTCCCATTTTCAT 3121
Qy 1045 GlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
Db 3122 CAGCAAGTTTGGAGAACCCACATTTTCTGCGCGTCACTCTGACAGGCGCTCCCTC 3181
Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
Db 3182 TGTCTACTCCATCTCTGAAAGCAAGACGAGGAGTGTCTGGGGGCCAAGGGCGCGCC 3241
Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
Db 3242 GGCCCTCTGCCCTCCGAGCGCGTGCAGTGGCTGTGCCACCAAGCATTTCTCTCAAGCTG 3301
Qy 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
Db 3302 ACTGCACACGGTGCACCTACGTGGCCACTCTTGGGGTCACTCAGGACAGCCAGACCGAG 3361
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
Db 3362 CTGAGTCGGAAGCTCCCGGGGAGACGCTGACTGCCCTGGAGGCCGAGCAACCCGGCA 3421
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
Db 3422 CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451

RESULT 5
US-09-572-423B-3
; Sequence 3, Application US/09572423B
; Patent No. 6331399
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William A. Gaarde
; APPLICANT: Edward Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0462
; CURRENT APPLICATION NUMBER: US/09/572,423B
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-572-423B-3

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.64% Indels: 0
DB: 4 Gaps: 0
US-08-951-733-20 (1-1154) x US-09-572-423B-3 (1-4015)
Qy 5 GlnArgCysValLeuLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
Db 2 CAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGACACCCCGCGATGCGG 61
Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTGCGGAGCGGTGCTCCCTGCTGCGCAGCCACTACCGCAGGCTGCTG 121
Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGCTGCCACGTTCGTGCGCGCGCTGGGGCCCCAGGCGTGGCGGTGGTGGCAGCGGG 181
Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTirPaspAla 84
Db 182 GACCCGCGCGCTTTCCGCGCGCTGTGTGGCCAGTGCCTGGTGTGCTGCTGCCCTGGGACGCA 241
Qy 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCCCCCGCGCGCCCCCTCTCCGCGAGGTGCTTGCCTGAAGGAGCTGGTGCC 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTCTCAGAGCGCTGTGCGAGCGCGCGCGAAGAACGCTGTGGCTTCGGCTTCGCG 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGTGTGACGGGGCGCGGGGGCCCCCGGAGGCTTCACACAGCGTGCAGAGTAC 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg 164
Db 422 CTGCCCCAACCGGTGACCGACGCTGTGGTTCACCTGTGCGCACGCTGCGCGCTCTTTGTCTGCG 481
Qy 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
Db 482 CGCGTGGCGACGACGCTGTGGTTCACCTGTGCGCACGCTGCGCGCTCTTTGTCTGCGTG 541
Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGCGCTTACCAGGTGTGCGGGCGCGCGCTGTACACAGCTGCGGCTGCCACT 601
Qy 205 GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
Db 602 CAGGCCCGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGCGGCC 661
Qy 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
Db 662 TGGAAACCATAGCGTCAGGAGCGCGGGTCCCTTGGGCGCTGCGAGCCCGGGTGGAGG 721
Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264
Db 722 AGCGCGGGGCGAGTGCAGCCGAAGTCTGCGGTGCGCAAGAGGCCAGCGCGTGGCGCT 781
Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
Db 782 GCCCTTGAGCGGAGCGACGCCCGCTTGGGACAGGGGTCTTGGGCCACCGCGGCGAGCG 841
Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluGluAla 304
Db 842 CGTGGACCGAGTGACCGTGGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901
Qy 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324
Db 902 ACCTCTTGGAGGGTGGCTCTCTGCGACGCGCCACTCCACCATCTCGTGGGCGCGCGAG 961
Qy 325 HisHisAlaGlyProProSerThrSerArgProProArgProTirPaspThrProCysPro 344
Db 962 CACCACGGGGCCCCCATCCACATCCAGTCCCGGCCACCATCTCCCTGGGACACGCTTGTCCC 1021

| | | | | |
|----|------|--|------|--|
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluInLeuArg | 364 | |
| Db | 1022 | CCGGTGTACCCGAGACCAAGCACTTCTCTACTCTCAGGCACAGAGAGCACTGCGG | 1081 | |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 | |
| Db | 1082 | CCCTCCTCTCTACTCAGCTCTCTGAGGCCAGCAGCTGACTGGCGCTCGAGGCTCGTGAG | 1141 | |
| QY | 385 | ThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuProArgLeu | 404 | |
| Db | 1142 | ACCATCTTCTGGGTTCAGGCCCTGGATGCCAGGACCTCCCGCAGGTTGCCCGCCCTG | 1201 | |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 | |
| Db | 1202 | CCCCAGGCTACTGCCAATGCGCCCTGTTCTGGAGCTGTTGGGAACACAGCGCAG | 1261 | |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 | |
| Db | 1262 | TGCCCCCTACGGGGTGTCTCTCAAGAGCAGCTGCCCGCTCGAGCTGGGTCACCCAGCA | 1321 | |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464- | |
| Db | 1322 | GCCGGTGTCTGTCCCGGGAGAACCCCAAGGGCTCTGTGGCGGCCCCCGAGGAGGAGAC | 1381 | |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGlnValTyr | 484 | |
| Db | 1382 | ACAGACCCCGCTCGCTGGTGACGTCTCCCGCAGCACAGACCCCTGGCAGGTGTAC | 1441 | |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProGlyLeuTrpGlySerArgHis | 504 | |
| Db | 1442 | GGCTTGTGGGGCTGCCTGCGCGCTGGTGGCCCGCAGGCTCTGGGGCTCCAGGSCAC | 1501 | |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 | |
| Db | 1502 | AAGCAAGCGCGCTTCTCAGGAACACCAAGAAGTTCTCTCCGTGGGAAGCATGCCAAG | 1561 | |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpIleuArgArg | 544 | |
| Db | 1562 | CTCTCGCTCAGGAGCTGACGTGGAGATGAGCGTGGGAGCTGCGCTGGCTGCCAGG | 1621 | |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla | 564 | |
| Db | 1622 | AGCCAGGGGTTGGCTGTGTTCGGCGCGCAGACACCGTCTCGGTGAGGAGATCCTGGCC | 1681 | |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr | 584 | |
| Db | 1682 | AAGTCTGCACGTGGCTGATGATGTACGTGCTCAGCTGCTCAGGTCTTCTTTAT | 1741 | |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 | |
| Db | 1742 | GTACCGAGACACCGTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGC | 1801 | |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 | |
| Db | 1802 | AAGTTCGAAGCATTTGGAATCAGACAGCAGCTTGAAGAGGTGCAGCTGGGGAGCTGTCG | 1861 | |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 | |
| Db | 1862 | GAAAGAGAGGTACGAGCAGCATCGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCGC | 1921 | |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyVala | 664 | |
| Db | 1922 | TTCATCCCAAGCTCAGCGGCTGCGCGCGATGTGAACATGACGTACGTCTGGGAGCC | 1981 | |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 | |
| Db | 1982 | AGAACGTTCCGAGAGAAAAGAGGCCGAGCGTCTCACCTCGAGGCTGAAGGCACGTTC | 2041 | |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 | |
| Db | 2042 | AGCGTCTCAACTACAGCGGGCGCGCGCCCGCTCTGGGGCCCTCTGTGTGGGC | 2101 | |
| QY | 705 | LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 | |
| Db | 2102 | CTGGACGATATCCACAGGGCTGGCGCACCTTGTGTGTGTGTGTGGGGCCAGGACCG | 2161 | |
| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 | |
| Db | 2162 | CCGCCCTGAGCTGTACTTGTCAAGTGTGATGTACGGGCGGTACGACACCATCCCCAG | 2221 | |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 | |
| Db | 2222 | GACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGGCT | 2281 | |
| QY | 765 | ArgTyrAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 | |
| Db | 2282 | CGGTATGCGGTGTCCAGAAGGCCCGCATGGCAGCTGCCGAAGGCTTCAAGAGCCAC | 2341 | |
| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 | |
| Db | 2342 | GTCTCTACCTTGACAGACCTCCAGCGCTACATGCAGCTTCTGTGGCTCACCTGCAGGAG | 2401 | |
| QY | 805 | ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 | |
| Db | 2402 | ACCAGGCCGCTGAGGATGCCGTGTCATCGAGCAGAGCTCTCCCTGATAGGCCAGC | 2461 | |
| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly | 844 | |
| Db | 2462 | AGTGGCTCTTCCAGCTTCTTCTACGCTTCTGTGCCACACCGCGGTGCCGTCAGGGGC | 2521 | |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 | |
| Db | 2522 | AAGTCTACCTCCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTGC | 2581 | |
| QY | 865 | SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 | |
| Db | 2582 | AGCTTGTCTTACGGCGACATGAGAGAACAGCTTTTTCGGGGATTCGGCGGGAGGCTG | 2641 | |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHisAlaLysThr | 904 | |
| Db | 2642 | CTCTCGGTTTGGTGGATGATTTCTTGTGTGTGACACCTCACCTCACCGCGGAAACCC | 2701 | |
| QY | 905 | PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 | |
| Db | 2702 | TTCTCTCAGGACCTGGTCCAGGTGTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 2761 | |
| QY | 925 | ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet | 944 | |
| Db | 2762 | ACAGTGGTGAACTTCCCTGTAGAGAGAGAGGCGCTGGGTGGCAGGCTTTTGTTCAGATG | 2821 | |
| QY | 945 | ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal | 964 | |
| Db | 2822 | CCGGCCACGGCCCTATTCCTTGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 2881 | |
| QY | 965 | GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg | 984 | |
| Db | 2882 | CAGAGGACTTACTTCCAGCTATGCCCGGACCTCCATCAGAGCCAGCTCTCACCTTCAACCGC | 2941 | |
| QY | 985 | GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys | 1004 | |
| Db | 2942 | GGCTTCAAGGCTGGGAGAACATGCGTGCAGAACTCTTTGGGGTCTTGGCGGCTGAAGTGT | 3001 | |
| QY | 1005 | HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr | 1024 | |
| Db | 3002 | CACAGCCTGTTTCTGGATTTGACAGGTGAACAGGCTCCAGAGCGGTGTGCACCAATCTAC | 3061 | |
| QY | 1025 | LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis | 1044 | |
| Db | 3062 | AAGATCTCTCTGTGAGGCGTACAGGTTTTCAGCGATGTGTGTGAGCTGCCATTTTCAT | 3121 | |
| QY | 1045 | GlnGluValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu | 1064 | |
| Db | 3122 | CAGCAGTTTGAAGAACCCACATTTTCTCGCGCTCATCTCTGACAGCGGCTCCCTC | 3181 | |
| QY | 1065 | CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla | 1084 | |

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Db      3182  TGCTACTCCATCTCTGAAAGCCAAAGACGACGAGGATGTCGTGGGGGCCAAAGGGCGCGCC 3241
Qy      1085  GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
Db      3242  GGCCCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTG 3301
Qy      1105  ThrArgHisArgValThrTrpValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
Db      3302  ACTCGACACCGTGTCACTACGTAGTGCCACTCCTGGGTCACTCAGGACAGCCACAGCGCAG 3361
Qy      1125  LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
Db      3362  CTGAGTCGGAGATCCCGGGGACGACCTGACTGCCCCGTGGAGCGCGCAACCCGGCA 3421
Qy      1145  LeuProSerAspPheLysThrIleLeuAsp 1154
Db      3422  CTGCCCTCAGACTTCAAGACCATCCTGGAC 3451

RESULT 6
US-09-128-354-1
; Sequence 1, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310US
; CURRENT APPLICATION NUMBER: US/09/128,354
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-128-354-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 4 Gaps: 0

US-08-951-733-20 (1-1154) x US-09-128-354-1 (1-4015)

Qy      5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24

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| | | | |
|----|------|---|------|
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgLeuProArgLeu | 404 |
| Db | 1142 | ACATCTTCTGGGTTCAGGCCCTGGATGCCAGGACTCCCGCAGGTGGCCGCGCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCCAGCGTACTGGCAATGCGGCCCTGTTCTGGAGCTGTTGGGAACACCGCGCAG | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCCCTACGGGTGCTCTCAAGACGCACTCCCGCTCGAGCTCGCGTCAACCCAGCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| Db | 1322 | GCCGGTGTCTGTCGCCGGAGAACCCCGAGGCTCTGTGGCGGCCCGCCGAGGAGGAC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| Db | 1382 | ACAGACCCCGCTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTAC | 1441 |
| QY | 485 | GlyPheValAlaCysLeuArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| Db | 1442 | GGCTTCGTGCGGGCTGCTGCGCGGCTGGTGCCTCCAGGCTCTGCGGCTCCAGGCAC | 1501 |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 |
| Db | 1502 | ACGAAAGCGCTTCTTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAAG | 1561 |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 |
| Db | 1562 | CTCTCGCTCAGGAGCTGACGTGGAAGATGACGCTGGCGGACTGCGCTTGGCTGGCAGG | 1621 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIleLeuAla | 564 |
| Db | 1622 | AGCCAGGGGTGGCTGTCTCCGCGCAGACACCGCTCTCGTGAGAGATCTCTGGCC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr | 584 |
| Db | 1682 | AAATTCTGCTGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTAT | 1741 |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| Db | 1742 | GTACGGAGACACCTTTCAAAGAACAGGCTCTTTTCTACCGGAAGATGCTGGAGC | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgLeuSer | 624 |
| Db | 1802 | AAATTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGGTGCAGCTGCGGAGCTGCG | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| Db | 1862 | GAAGCAGAGGTTCAGGAGCATCGGAAGCCAGCGCCGCTGCTGACGTCCAGACTCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| Db | 1922 | TTTCATCCCAAGCTTCAGCGGTGCGCGCATGTGTGAACATGCATACGTCTGGGAGCC | 1981 |
| QY | 665 | ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| Db | 1982 | AGAAGCTTCCGAGAGAAAAGGCGGAGCGTCTCACCTCGAGGGTGAAGCACTGTTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
| Db | 2042 | ACCGTGCTCACTACAGCGCGCGCGCCCGCCGCTCTGTCGGCGCTCTGTCGGGC | 2101 |
| QY | 705 | LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 |
| Db | 2102 | CTGGAGATATCCACAGGCGCTGGCGACCTTCTGCTGCTGCTGTCGGCGCTCTGTCGGC | 2161 |
| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyValTyrAspThrIleProGln | 744 |
| Db | 2162 | CGCCCTGAGCTGTACTTGTCAAGTGGATGTGACGGGCGCTACGACACCATCCCCAG | 2221 |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 |
| Db | 2222 | GACAGGCTCAGGAGGTGATCGCCAGCATCAAAACCCAGAACACGACTCGTGGCTG | 2281 |
| QY | 765 | ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
| Db | 2282 | CGGTATGCGTGGTCCAGAAGCGCCCATGGCAGCTCCGCAAGGCCCTCAAGAGCCAC | 2341 |
| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 |
| Db | 2342 | GTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGAGGAG | 2401 |
| QY | 805 | ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 |
| Db | 2402 | ACCAGCCCTCAGGGATCGGTGTCATGCGACAGAGTCTCTCCCTGAATGAGGCAGC | 2461 |
| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly | 844 |
| Db | 2462 | AGTGGCTCTTCGACGCTCTCTCTAGCTTTCATGTCGCCACACGCCCTGGCATCAGGGC | 2521 |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| Db | 2522 | AACTCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTCTGCTGC | 2581 |
| QY | 865 | SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgaspGlyLeu | 884 |
| Db | 2582 | ACCTGTGCTACGCGCACATGGAGAACAAGCTGTTTTCGGGGGATTTCGGGGGACGGGCTG | 2641 |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr | 904 |
| Db | 2642 | CTCTGCGTTCGTGGATGATTTCTTGTGTTGGTGACACCTCACCTCACCCACGGAACCC | 2701 |
| QY | 905 | PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 |
| Db | 2702 | TTCTCAGACACCTGCTCGAGGTGCTCTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTG | 2761 |
| QY | 925 | ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet | 944 |
| Db | 2762 | ACAGTGTGAACCTTCTCTGTAGAAGACGAGGGCCCTGGGTGGCACGCTTTTGTTCAGATG | 2821 |
| QY | 945 | ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal | 964 |
| Db | 2822 | CCGGCCACCGGCTATTCCTTCCTGGTGGCGGCTGCTGCTGGATACCCGCGACCTGGAGGTG | 2881 |
| QY | 965 | GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg | 984 |
| Db | 2882 | CAGAGCGACTACTCCAGCTATGCCGAGCTCTCCATCAGACGCACTCTCACCTTCAACCCG | 2941 |
| QY | 985 | GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys | 1004 |
| Db | 2942 | GGCTTCAAGGCTGGGAGAACATGCGTGCACAACTCTTTGGGCTCTTGGGCTGAAAGTGT | 3001 |
| QY | 1005 | HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr | 1024 |
| Db | 3002 | CACAGCTCTTCTGATTTGACAGTGAACAGGCTCCACAGGCTGACCAACATCTAC | 3061 |
| QY | 1025 | LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis | 1044 |
| Db | 3062 | AAAGTCTCTGCTGCGAGGTACAGGTTTTCAGCATGTGTGCTGCTGCTGCTGCTGCTGCTG | 3121 |
| QY | 1045 | GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu | 1064 |
| Db | 3122 | CAGCAAGTTTGAAGAACCCACATTTTCTCGCGCTCATCTCTGACACGCGCTCCCTC | 3181 |
| QY | 1065 | CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla | 1084 |
| Db | 3182 | TGCTACTCTCTTGAAGCCAAAGACGAGGATGTGCTGGGGGCCAAGGGCGCGCC | 3241 |
| QY | 1085 | GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu | 1104 |
| Db | 3242 | GGCCCTCTGCCCTCCGAGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 3301 |
| QY | 1105 | ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln | 1124 |

| | | | |
|----|------|---|------|
| Db | 3302 | ACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCGACGACG | 3361 |
| Qy | 1125 | LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla | 1144 |
| Db | 3362 | CTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGACCAACCCGCA | 3421 |
| Qy | 1145 | LeuProSerAspPheLysThrIleLeuAsp | 1154 |
| Db | 3422 | CTGCCCTCAGACTTCAGACCATCCTGGAC | 3451 |

RESULT.7

```

US-09-675-321-1
; Sequence 1, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)

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| Alignment Scores: | |
|------------------------|---------|
| Pred. No.: | 0 |
| Score: | 6057.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 99.64% |
| DB: | 4 |
| Gaps: | 0 |
| Indels: | 0 |
| Mismatches: | 0 |
| Conservative: | 0 |
| Matches: | 1150 |
| Length: | 4015 |

US-08-951-733-20 (1-1154) x US-09-675-321-1 (1-4015)

| | | | | |
|----|--|-----|--|-----|
| QY | | 5 | GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro | 24 |
| Dd | | 2 | CAGCGCTGCCTGCTCGCACGTGGGAACCCCTGGCCCCGCCACC | 61 |
| QY | | 25 | ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu | 44 |
| Dd | | 62 | CGCGTCCCCTGTCGCGAGCGTGCGTCCCTGTCGCAGCCACTACCGCAGAGTGCTG | 121 |
| QY | | 45 | ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly | 64 |
| Dd | | 122 | CCGCTGGCCAGTTCGTGCGCGCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGCGGG | 181 |
| QY | | 65 | AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTPrAspAla | 84 |
| Dd | | 182 | GACCCGGCGGCTTTCCGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCCTCGCCCTGGGAGCCA | 241 |
| QY | | 85 | ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla | 104 |
| Dd | | 242 | CGGCGCGCCCGCGCGCCCTCCTTCCTCCGCAAGTGTCTCTGCTGAAGAGCTGGTGGCC | 301 |
| QY | | 105 | ArgValLeuGlnArgLeuCysGluArgGlyAlaIlysasnValLeualaPheGlyPheAla | 124 |
| Dd | | 302 | CGAGTGTGCAGAGGCTGTGCGAGCGCGGCCAAGAACGTGTCGCTTCGGCTTCGGTTCGGG | 361 |

| | | | |
|----|------|--|------|
| QY | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr | 144 |
| Db | 362 | CTGCTGGACGGGGCCGGGGGGCCCCCGGAGGCGCTTACACACGAGCGTGGCAGCTAC | 421 |
| QY | 145 | LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg | 164 |
| Db | 422 | CTGCCCAACACGGTACCGACACACTGGGGGGAGCGGGCGTGGGGGTGCTGCTGGCGC | 481 |
| QY | 165 | ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal | 184 |
| Db | 482 | CCGCTGGGGACAGAGTCTGTGTTCACTGCTGGCACGCTGGCGCGCTCTTTGTGCTGGT | 541 |
| QY | 185 | AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr | 204 |
| Db | 542 | GCTCCAGCTGGCGCTACCAAGTGTGGGGCGCGCTGTACCACTCTGGCGCTGCCACT | 601 |
| QY | 205 | GlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla | 224 |
| Db | 602 | CAGGCCCGCGCCCCGCCACACGCTAGTGGACCCCGAAGCGCTGGGATGCGAACGGGCC | 661 |
| QY | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| Db | 662 | TGGAAACCATAGCGTCAGGGAGCCGGGTGCCCTTGGGCCCTGCCAGCCCGGGTGGAGG | 721 |
| QY | 245 | ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgTrpArgArgGlyAla | 264 |
| Db | 722 | AGGCGGGGGCAGTGCAGCGAGTCTGCCGTGTGCCACAGAGGCCACGGCGTGGCGCT | 781 |
| QY | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| Db | 782 | GCCCTGTAGCGGGAGCGACGCCCTTGGGACAGGGTCTCTGGGCCACCGCGGACGAGC | 841 |
| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| Db | 842 | CGTGACCGAGTGAACGTGGTTCTGTGTGTGTACCTGCCACACCGCGCGAAGAGCC | 901 |
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| Db | 902 | ACCTCTTTGGAGGTGGCTCTCTGGCACGGCCACTTCCACCCATCGTGGCGCCGAC | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| Db | 962 | CACCACGGGGCCCCCATCCACATCGCGGCACACACGTCCTCGGACACGCTTGTCCT | 1021 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| Db | 1022 | CCGCTGTAGCCCGAGACCAACACTTCTCTACTCTCTCAGGCGACAGGACGCTGGG | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| Db | 1082 | CCCTCTTCTTACTCAGCTCTCTCAGAGCCACGCTGACTGGCGCTCGGAGGCTCGTGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| Db | 1142 | ACCATCTTCTTGGGTCTCAGGCCCTTGGATGTCAGGGACTCCCGCAGGTTGCCCGCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCCAGCGCTACTGGCAAAATCGCGCCCTGTCTCTGGAGTGTCTTGGGAACACGCGCAG | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCTTACGGGGTCTCTCAAGACGACTGCCCGTGGAGTGGGGTCACCCCAGCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| Db | 1322 | GCGCGTCTCTGTGCCCGGGAGAGCCCGCGGCTCTGTGGCGGCCCGCAGGAGGAGC | 1381 |
| QY | 465 | ThrAspProArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| Db | 1382 | ACAGACCCCGTGCCTGGTGGAGTCTCTCGGCAGCACAGACGCCCTGGCAGGTGCTAC | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuLeuArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |

1442 GGCCTTCGTGGGGCTGCTGCGCGGCTGGTGGCCCCCAGGCGCTCGGGGCTCAGGCAC 1501
505 AsnGluArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHisAlaLys 524
1502 AACGAAGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAG 1561
525 LeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaTyrLeuArgArg 544
1562 CTCTCGCTGCAGGAGCTGACGTGGAGATGAGCGTGGGGACTCGCGCTGGCTGGCGAGG 1621
545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla 564
1622 AGCCAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTCGCTGAGGAGATCCTGGCC 1681
565 LysPheLeuHisTyrLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr 584
1682 AAGTTCCTGCACTGGCTGATGAGTGTACGTCTGAGCTGCTCAGGTCTTCTTTTAT 1741
585 ValThrGluThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerValTyrSer 604
1742 GTACAGGAGACCATGTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTGTCTGGAGC 1801
605 LysLeuGlnSerIleGlyLysLeuGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
1802 AAGTTGCAAGCATTTGAATCAGACACGACTTGAAGAGGTGACGTGCGGGAGCTGTGG 1861
625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
1862 GAAGCAGAGGTTCAGCAGCATCGGGAAGCCAGGCGCCCTGCTGCTGACGTCCAGACTCCG 1921
645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664
1922 TTATATCCCAAGCTGACGGCTCGGCCGATTGTGAACATGAGTACGTCTGGGAGCC 1981
665 ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
1982 AGAAGCTTCGCAGAGAAAGAGGGCGGAGCGTCTACCTCGAGSGTGAAGGCACCTGTC 2041
685 SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704
2042 AGCTGTCTCACTACGAGCGGCGCGCGCCCGCTGCTGGCGGCTCTGTGCTGGGC 2101
705 LeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGlnAspPro 724
2102 CTGGACCATATCCACAGGCGCTGGCGACCTTCGTGCTGCTGGCGGCGCCAGACCG 2161
725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
2162 CCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGCGCGGTACGACACCATCCCCAG 2221
745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764
2222 GACAGGCTCAGGAGGTTCATCGCCAGCATCATCAACCCCAAGACACGTACTGCTGGCT 2281
765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
2282 CGGTATCCGTGGTCCAGAGGCGCCCATGGGCGCGTCCCAAGGCGCTTCAAGAGCAC 2341
785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804
2342 GTCTCTACCTTGCAGACACCTCCAGCCGTACATGGACAGATTCGTGGCTCACTGCAGGAG 2401
805 ThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGluAlaSer 824
2402 ACCAGCCGCTGAGGATGCGCTGCTCATCGACAGAGCTCTCCCTGAATGAGCGCAGC 2461
825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
2462 AGTGGCTCTTCGACGCTTCCTACGCTTATGTCACACGCGCGTGGCATCAGGGGC 2521
845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864

2522 AAGTCTACGTCCAGTCCAGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTGC 2581
865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
2582 AGCTGTCTACGGCGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGAGCGGCTG 2641
885 LeuLeuArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
2642 CTCTCGCTTGGTGGATGATTTCTGTTGGTGACCTCACCTCACCCAGCGCAAAACC 2701
905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValIleAsnLeuArgLys 924
2702 TTCCTCAGGACCCCTGGTCCGAGGTGCTCCCTGAGTATGCTGCGTGTGAACCTTCGCGAAG 2761
925 ThrValValAsnPheProValGluAspGluAlaLeuGlyLysThrAlaPheValGlnMet 944
2762 ACAGTGGTGAACCTTCCCTGTAGAACAGAGGCGCTGGGTGGCAGCGCTTTGTTTTCAGATG 2821
945 ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964
2822 CCGGCCACGCGCTATTCCTCGTGGCGCTGCTGCTGGATACCCCGACCCCTGGAGGTG 2881
965 GlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984
2882 CAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCGAGTCTCACCTTCACCGC 2941
985 GlyPheLysAlaGlyArgAsnMetArgLysLeuPheGlyValLeuArgLeuLysCys 1004
2942 GGCTTCAAGGCTGGGAGAACATGCTGCGCAAACTCTTTGGGGTCTTGGCGTGAAGTGT 3001
1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
3002 CACAGCTGTGTTCTGGATTTGAGGTGAACAGCTCCAGAGCGGTGTCACCAACATCTAC 3061
1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
3062 AAGATCTCTCTGCTGCGAGCGTACAGGTTTTCACGCATGCTGTGCTGACGCTCCCATTTT 3121
1045 GlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
3122 CAGCAAGTTTGGAGAACCACACATTTTTCCTGCGCGTCACTCTCTGACACGCGCTCCCTC 3181
1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGlyAlaAla 1084
3182 TGCTACTCCATCTCGAAAGCCAGAACCGAGGATGTCCTGGGGGGCCAGGGCGCCGCC 3241
1085 GlyProLeuProSerGluAlaValIleThrLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
3242 GGCCCTCTGCGCTCCGAGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTG 3301
1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
3302 ACTGCACACCTGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3361
1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
3362 CTGAGTCGAAGCTCCCGGGAGCAGCGCTGACTGCCCTGGAGGGCGCGCAGCAACCCGCA 3421
1145 LeuProSerAspPheLysThrIleLeuAsp 1154
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RESULT 8

US-09-052-919-1

; Sequence 1, Application US/09052919

; Patent No. 6444650

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 | QY | 665 | ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| DB | 902 | ACCTCTTGGAGGGTGGCTCTCTGGCAGCGCCACTCCACCCATCCGTGGCGCCGAC | 961 | DB | 1982 | AGAAAGTTCGCGAGAGAAAGAGGCGGAGCTCTACCTCGAGGTGAAGCACTGTC | 2041 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 | QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
| DB | 962 | CACCACGGGGCCCCCATCCACATCGCGCCACCACTCCCTGGGACACGCTGTGCC | 1021 | DB | 2042 | ACGGTGCTCAACTACGAGCGGGCGGCGCCCGGCGCTCCTGGCGCCTCTGTGCTGGGC | 2101 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluLeuArg | 364 | QY | 705 | LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 |
| DB | 1022 | CGGGTGACGGCGAGCAAGCACTTCTCTACTCTCAGGGGACAAAGAGCAGCTGGG | 1081 | DB | 2102 | CTGGAGCATATCCACAGGGCCTGGCGACCTTCGTGCTGCTGGCGCCAGGACCG | 2161 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 | QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 |
| DB | 1082 | CCCTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTCGTGAG | 1141 | DB | 2162 | CGCGCTGAGCTGACTTTGTCAAGGTGGATGTGACGGGCGGTACACACCATCCCCCAG | 2221 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 | QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 |
| DB | 1142 | ACCATCTTCTGGTTCAGGCCCTGGATGCCAGGACTCCCGCAGGTGGCCCGCCTG | 1201 | DB | 2222 | GACAGGCTCACGGAGTCTATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGGT | 2281 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHisAlaGln | 424 | QY | 765 | ArgTyrAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
| DB | 1202 | CCCCAGCGTACTGGCAATCGCGCCCTGTCTCTGGAGCTGCTTGGAAACACACGCGAG | 1261 | DB | 2282 | CGGTATGCGGTGGTCCAGAAGGCGGCCCATGGCGACGTCCGCAAGGCTTCAAGAGCCAC | 2341 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 | QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 |
| DB | 1262 | TGCCCCCTACGGGGTGTCTCTAAGACGCACTGCCCGCTGCGAGCTGCCGCCAGCA | 1321 | DB | 2342 | GTCTCTACCTTGACAGACCTCCAGCGGTACATGCGGACGTTCGTGGCTCACCTGCAGGAG | 2401 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 | QY | 805 | ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 |
| DB | 1322 | GCCGGTGTCTGCGCCGGAGAACCCCGAGGCTGTGGCGGCCCGCCGAGGAGGAC | 1381 | DB | 2402 | ACCAGCCGCTCAGGGATCCGCTGCTCATCGAGCAGAGCTCTCTCCCTGATGAGGCCAGC | 2461 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 | QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly | 844 |
| DB | 1382 | ACAGACCCCGCTGCGCTGGTGAGCTGTCCGCCAGCACAGCAGCCCTGGCAGGTGAC | 1441 | DB | 2462 | AGTGGCTCTTCGAGCTCTCTCTAGCTTCTATGTGCACACGCGCTGCGCATCAGGGGC | 2521 |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 | QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| DB | 1442 | GGCTTCGTGGGGCTGCTGCGCGGTGGTGGCCCCCAGAGGCTCTGGGGCTCCAGGCAC | 1501 | DB | 2522 | AAGTCTCAGTCCAGTGCCAGGGGATCCCGCAGGGGTCTCATCTCTCCACGTGCTCTGC | 2581 |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 | QY | 865 | SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 |
| DB | 1502 | AACGAACCGCTCTCCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAAG | 1561 | DB | 2582 | AGCTGTGCTACGGCGACATGAGAACAGCTGTTTGGGGGATTCGGCGGACGGGCTG | 2641 |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 | QY | 885 | LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr | 904 |
| DB | 1562 | CTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTCCGGGACTGCGGCTGGCGCAGG | 1621 | DB | 2642 | CTCCTCGCTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCAAAACC | 2701 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIleLeuAla | 564 | QY | 905 | PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 |
| DB | 1622 | AGCCAGGGGTGGCTGTGTCCGGCGCGAGAGCACCGTCTCGTGAGGAGATCCTGGCC | 1681 | DB | 2702 | TTCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGGCTGGGTGGTGAACCTGGCGAAG | 2761 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr | 584 | QY | 925 | ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet | 944 |
| DB | 1682 | AGTTCTCTGCACTGGCTGATGAGTGTACGTCTGCTGAGCTGCTCAGGTCTTCTTTAT | 1741 | DB | 2762 | ACAGTGGTGAACCTCCCTCTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGATG | 2821 |
| QY | 585 | ValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 | QY | 945 | ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal | 964 |
| DB | 1742 | GTACGGAGACACCGTTTCAAAAGAACAGCGCTCTTTTCTACCGGAAGAGTCTCTGGAGC | 1801 | DB | 2822 | CGGGCCACGGCTATTCCCTCGTGGCGGCTGCTGCTGATACCCGACCCCTGGAGGTG | 2881 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 | QY | 965 | GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg | 984 |
| DB | 1802 | AGTTTGCAAGCATTTGAATCAGACGACCTTGAAGAGGGTGCAGCTCGGGAGGTGTCG | 1861 | DB | 2882 | CAGAGCAGTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCCG | 2941 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 | QY | 985 | GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys | 1004 |
| DB | 1862 | GAAGCAGAGGTGAGCAGCATCGGAAGCAGCCAGGCCCGCCCTGCTGCTGCTGAGCTCCG | 1921 | DB | 2942 | GGCTTCAAGGCTGGAGGAGACATGCTGCCAAACCTTTTGGGGTCTTGGCGGTGAAGTGT | 3001 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 | QY | 1005 | HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr | 1024 |
| DB | 1922 | TTTCATCCCAAGCTTGACGGGTGCGCGCGATGTGTGAACATGAGTACTGCTGCTGGAGCC | 1981 | DB | 3002 | CACAGCTCTTCTGATTTGCAGGTGAAACGCTCCACAGCGGTGCGACCAACATCTAC | 3061 |
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Db 3062 AAGATCCTCTGCTGCAGGCGTACAGGTTTCACGCATGTGCTGCAGCTCCCATTCAT 3121
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Db 3122 CAGCAAGTTTGGAGAAGCCACACATTTTCTCGCGCTCATCTCTGCACGGCTCCCTC 3181
Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaLa 1084
Db 3182 TGCTACTCCATCCCTGAAAGCAAGACGACAGGATGTCGTGGGGGCAAGGGCGCGCC 3241
Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
Db 3242 GGCCCTCGCCCTCCGAGGCGTGCACTGGCTGTGCCCAAGATTCTCTGCTCAAGCTG 3301
Qy 1105 ThrArgHisArgValThrTrpValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
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RESULT 9

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; Sequence 1, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTERT"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hTERT) catalytic protein
; OTHER INFORMATION: component"
; US-08-912-951-1
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Alignment Scores:

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Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 4 Gaps: 0

US-08-951-733-20 (1-1154) x US-08-912-951-1 (1-4015)
Qy 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
Db 2 CAGCGCTGCGTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGGCCACCCCGCGATGCCG 61
Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGTCGCGACGCCACTACCGCGAGGTGCTG 121
Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGCTGGCCACGTTCTGTCGCGCGCTGGGGCCCCCAGGGCTGGTGTGACGCGGGG 181
Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCGGGCGCTTTCGCGGGCTGGTGGCCAGTCGCTGGTGGCGTGCCTTGGGACGCA 241
Qy 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGCGCGCCCGCCCGCCCTCTCTCCGCGAGGTGCTCTCCCTGAAGGAGCTGGTGGCC 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTCTGAGAGGCTGTGCGAGCGCGCGGCGGGAAGAACGTGTGGCTTCGCGT 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGGACGGGCGCGGGGGCCCCCGAGGCTTTCACCAACCGCTGGCGAGGTAC 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
Db 422 CTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGGCTGTGCTGCTGCGC 481
Qy 165 ArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
Db 482 CGCGTGGGCGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
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| QY | 185 | AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr | 204 |
| Db | 542 | GCTCCAGGTGGCTTACCAGGTGTGCGGGCGCGCTGTACAGTCCGCGCTGCCACT | 601 |
| QY | 205 | GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla | 224 |
| Db | 602 | CAGGCCGCGCCGCCACACGCTAGTGACCCCGAAGGCGTGGGATGCCAGCGGC | 661 |
| QY | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| Db | 662 | TGGAACATATAGGTCAGGGAGGCGGGTCCCGCTGGCGCTGCCAGCCCGGGTGGAGG | 721 |
| QY | 245 | ArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProArgGlyAla | 264 |
| Db | 722 | AGCGCGGGGGCAGTGCCAGCGAGTCTGCGTTGCCAAGAGGCCAGGCGTGCGCT | 781 |
| QY | 265 | AlaProGluProGluAlaGlyThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| Db | 782 | GCCCTGAGCGGAGGAGCGCCGCTTGGGCAGGGGTCTTGGGCCACCCCGGCGAGGCG | 841 |
| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| Db | 842 | CCTGGACCGAGTGACCGTGGTTCTGTGTGTGTCACTGCCAGACCCCGCGAAGAGCC | 901 |
| QY | 305 | ThrSerLeuGluAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| Db | 902 | ACCTCTTGGAGGGTGGCTCTGTGGCAGCGGCCACTCCACCCTATCCGTGGCGGCCAG | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| Db | 962 | CACCAGCGGGCCCCCATCCACATCGCGGCCACACACGTCCTTGGGACACGCTGTGCC | 1021 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| Db | 1022 | CGGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAAGGAGCAGT | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| Db | 1082 | CCCTCTTCTACTCAGCTCTCTGAGGGCCACGCTGACTGGCGCTCGGAGGCTCGTGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| Db | 1142 | ACCATCTTCTGGTTCCAGGCCCTTGGATGCCAGGAGTCCCGCGAGGTTGCCCGCCG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGTTGGGAACACACGCGC | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCCCTAGGGGGTGTCTCTAAGAGCGCACTGCCGCTCGAGCTGCGGTCAACCCAGCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| Db | 1322 | GCCGGTGTGTGCCCCGGGAGAAGCCCCAGGCTCTGTGGCGGCCCGCCGAGGAGGAC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| Db | 1382 | ACAGACCCCGGTGCGCTGTGTGAGCTGTCTCCGCCACAGCAGCAGCCCTTGGCAGGT | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| Db | 1442 | GGCTTCGTGGGGCTGGCTGCGCGGCTGGTGGCCCCCAGAGGCTCTTGGGGCTCCAGG | 1501 |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 |
| Db | 1502 | AACGAACCGGCTTCTCAGGAACACCAAGAAGTTCATCTCCTTGGGGAAGCATGCCAAG | 1561 |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 |
| Db | 1562 | CTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGAGTGGCTTGGCTGGCGAGG | 1621 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIleLeuAla | 564 |
| Db | 1622 | AGCCCCAGGGTGGCTGTGTTCCGGCCGAGAGCACCGTGTGCTGAGGAGATCCTGGGC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr | 584 |
| Db | 1682 | AAGTTCTCGACTGGCTGATGAGTGTAGTGTGCTGAGTGTCTAGGCTCTTCTTTTAT | 1741 |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| Db | 1742 | GTACCGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAG | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyLeuArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 |
| Db | 1802 | AGTTTGCAAGCATTCGAATCAGACAGCACTTGAAGAGGCTGAGCTGGGGAGCTGTCG | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| Db | 1862 | GAAGCAGAGGTCCAGGACGATCGGGAAGCAGGCCCGCCCTGCTGACGTCCAGACTCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
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| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| Db | 1982 | AGAACGTTCCGCAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGACGTGTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
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| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 |
| Db | 2162 | CGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCCAG | 2221 |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 |
| Db | 2222 | GACAGGCTCAGCGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGGT | 2281 |
| QY | 765 | ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
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| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly | 844 |
| Db | 2462 | AGTGGCTCTTCGACGCTCTCTTACGCTTCTGTGCGCACACCGCCGTCATCAGGGGC | 2521 |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| Db | 2522 | AAGTCTCAGTCCAGTGCCAGGGATCCCGAGGGCTCCATCTCTCCAGCTGCTGCTGC | 2581 |
| QY | 865 | SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 |
| Db | 2582 | AGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGGGGATTCGGGGGAGCGGCTG | 2641 |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr | 904 |
| Db | 2642 | CTCCTCGCTTGTGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACCGCAAAAC | 2701 |
| QY | 905 | PheLeuArgThrLeuValValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 |

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Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
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; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733, 294A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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US-09-733-294A-3
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 4 Gaps: 0
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US-08-951-733-20 (1-1154) x US-09-733-294A-3 (1-4015)

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Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCGCGCGGCTTTCGCGCGCTGCTGGCCAGTCCCTGCTGCTGCGTGGTGGAGGCA 241
Qy 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCGCGCGCGCGCTCTCTCGCCAGAGTCTCTGCTGAAAGAGCTGGTGCC 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTGTCAGAGAGCTGTGCGAGCGCGCGCGGAGAACGTCGTGGCTTCGGCTTCG 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGGAGGGGCGCGCGGGGCGCCCGGAGCCTTACACACAGCGTGCAGCTAC 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
Db 422 CTGCCCCAACAGGTGACGACGACGCTCGGGGGAGCGGGGCTGCTGCTGCGC 481
Qy 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
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Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGCGCTTACCAGTGTGCGGGCGCGCGCTGTACACAGCTCGCGCTGCCACT 601
Qy 205 GlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
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Qy 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyValArg 244
Db 662 TGGAAACCATAGCTCAGGGAGCGCGGGTCCCGCTGGCGCTGCGAGCCCGGGTGGCAGG 721
Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264
Db 722 AGGCGCGGGGCGAGTGCACGCGAAGTCTGCCGTGTCAGAGAGCCAGCGCGTGGCGCT 781
Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
Db 782 GCCCTGAGCGGGAGCGAGCGCGCTTGGGCGAGGGTCTTGGGCGGCCACCCGCGGAGGAC 841
Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304
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|----|------|---|------|--|
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 | |
| Db | 902 | ACCTCTTTGGAGGTTGCGCTCTCTGCGACGCCCACTCCACCAATCCGTCGGCGGCCAG | 961 | |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 | |
| Db | 962 | CACCACGGGGCCCCCATCCACATCGGGGCCACACAGGTCCTCGGACACGCTTGTCCC | 1021 | |
| QY | 345 | ProValTyrAlaGluThrIysHisPheLeuTyrSerSerGlyAspIysGluGlnLeuArg | 364 | |
| Db | 1022 | CCGGTGTAGCCGAGAACCAAGCACTTCTCTACTCCTTCAGGGCGACAAGGAGAGTGGG | 1081 | |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 | |
| Db | 1082 | CCCTCTCTCTACTCAGCTCTCTGAGGCCCAACCTGACTGGCGCTCGGAGGCTGTGGAG | 1141 | |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 | |
| Db | 1142 | ACCATCTTTCTGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCTG | 1201 | |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 | |
| Db | 1202 | CCCCAGCGCTACTTGCAATCGCGCCCTGTTTCTTGGAGCTGTTGGGAACACACGCGCAG | 1261 | |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 | |
| Db | 1262 | TGCCCTACCGGGTGTCTCTCAAGACGCACTGCCGCTCGAGCTCGCGTCAACCCAGCA | 1321 | |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 | |
| Db | 1322 | GCCGCTGTCTGTCGGGAGAACCCCAAGGCTCTGTGGCGGCCCCCGAGGAGGAC | 1381 | |
| QY | 465 | ThrAspProArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 | |
| Db | 1382 | ACAGACCCCGCTGCTGCGAGCTGCTCCGCCACACAGACAGACGCCCTTGGCAGGTGAC | 1441 | |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 | |
| Db | 1442 | GGCTTCGTCGGGCTGCTGCGCCGCGTGTGTCGCCCAAGGCTCTGGGGCTCCAGGCAC | 1501 | |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrIysLysPheIleSerLeuGlyLysHisAlaLys | 524 | |
| Db | 1502 | AACGAACGCGCTTCTCAGGAACACCAAGAAGTTCACTCTCCCTGGGGAAGCATGCCAAG | 1561 | |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 | |
| Db | 1562 | CTCTCGCTGCAGGAGCTCACGTGGAAGATGACGCTGCGGACTGCGCTTGGCTGGCGAGG | 1621 | |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla | 564 | |
| Db | 1622 | AGCCACAGGGTGGCTGTGTCGGCCGCGAGACACCGCTCTCGGTGAGAGATCCTGGCC | 1681 | |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr | 584 | |
| Db | 1682 | AAGTTCCTGCACTGGCTGATGATGTGTACGTGTCGAGCTGCTCAGGCTCTTCTTTAT | 1741 | |
| QY | 585 | ValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 | |
| Db | 1742 | GTACGGAGACACGCTTTCAAAGAACAAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAGC | 1801 | |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 | |
| Db | 1802 | AAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGGTGCG | 1861 | |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 | |
| Db | 1862 | GAAGCAGAGGTTCAGCAGCATCGGGAAGCCAGGCCGCCCTGCTGCTCAGACTCCAGCTCCG | 1921 | |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 | |
| Db | 1922 | TTATCCCCAACGCTTGACGGCTGCGGCCGATGTTGTAACATGAGTACGTCTGTGGAGCC | 1981 | |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 | |
| Db | 1982 | AGAACCTTCGAGAGAAAAGGGCCGAGCGTCTCACCTCGAGGCTGAAGGCACGTCTTC | 2041 | |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 | |
| Db | 2042 | AGCGTCTCAACTACGAGCGGGCGCGCCCGCCGCTCTCTGGCGCCTCTGTGCTGGGC | 2101 | |
| QY | 705 | LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 | |
| Db | 2102 | CTGGAGATATCCACAGGGCCTGGCGCACTTCTGCTGCTGCTGGGGGCCAGGACCCG | 2161 | |
| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTrpAspThrIleProGln | 744 | |
| Db | 2162 | CGCCCTGAGCTGTACTTGTCAAGGTGGATGTACGGGCGGTACGACCACTTCCCCACG | 2221 | |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg | 764 | |
| Db | 2222 | GACAGGCTCACGGAGGTATCGCCAGCATCATCAACCCCAAGACGACTCTCGTGGCT | 2281 | |
| QY | 765 | ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 | |
| Db | 2282 | CGGTATGCGTGGTCCAGAAAGCGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCCAC | 2341 | |
| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 | |
| Db | 2342 | GTCTCTACCTTGACAGACCTCCAGCGCTACATGCGACAGTTCGTGCTCACCTGCAGGAG | 2401 | |
| QY | 805 | ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 | |
| Db | 2402 | ACCAGCCGCTGAGGGATCGCTGCTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGC | 2461 | |
| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly | 844 | |
| Db | 2462 | AGTGGCTCTTCGACGCTCTCTACGCTTCTGTGTCACACGCGCTGGGCATCAGGGGC | 2521 | |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 | |
| Db | 2522 | AGTCTCTAGTCCAGTCCCGAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTC | 2581 | |
| QY | 865 | SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 | |
| Db | 2582 | AGCTGTGCTACGGCGACATGGAGAACAGCTGTTTTCGGGGATTCGGCGGAGCGGCTG | 2641 | |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr | 904 | |
| Db | 2642 | CTCCTGCGTTCGTGGATGATTTCTTGTGTCACACCTCACCTCACCCACGCAAAACC | 2701 | |
| QY | 905 | PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys | 924 | |
| Db | 2702 | TTCTCTCAGGACCTGTGTCGAGGTGCTCTGAGTATGGCTGGCTGAGTTCGCGAAG | 2761 | |
| QY | 925 | ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet | 944 | |
| Db | 2762 | ACAGTGGTGAACCTCCCTGTAGAGACAGGCGCTGGGTGGCACGGCTTTGTTCAAGTC | 2821 | |
| QY | 945 | ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal | 964 | |
| Db | 2822 | CGGGCCACGGCTATTCCCTGTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 2881 | |
| QY | 965 | GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg | 984 | |
| Db | 2882 | CAGAGCGACTACTCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCACCCGC | 2941 | |
| QY | 985 | GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys | 1004 | |
| Db | 2942 | GGCTTCAGAGCTGGGAGGACATGCTGCCAACTCTTTGGGGCTCTGGGGCTGAAGTGT | 3001 | |
| QY | 1005 | HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr | 1024 | |
| Db | 3002 | CACAGCTGTTCTTGGATTTGCAAGTGAACAGCTCCAGACGCTGTCACCAACATCTAC | 3061 | |
| QY | 1025 | LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis | 1044 | |

Db 3062 AAGATCCTCTCTGCTGAGGCGTACAGGTTTACAGCATGTGTGCTGAGCTCCCATTTTCAT 3121
Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
Db 3122 CAGCAAGTTTGGAAAGACCCACACATTTTCTGCGGTCATCTCTGACACGGCCTCCCTC 3181
Qy 1065 CysTrpSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
Db 3182 TGCTACTCCATCCCTGAAGCCCAAGACGACGAGATGTGCTGGGGCCCAAGGGCCGCC 3241
Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
Db 3242 GGCCCTCTGCCCTCCGAGGCGGTGAGTGGTGTGCCACCAAGCATCTCTCAAGGTG 3301
Qy 1105 ThrArgHisArgValThrTyValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
Db 3302 ACTCGACACCGGTGTCACCTAGTCCCACTCTCTGGGGTCACTCAGACGACGACGACG 3361
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
Db 3362 CTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTGGAGGCGGACCAACCCGGCA 3421
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
Db 3422 CTGCCCTCAGACTTCAAGACCATCTCGAC 3451

RESULT 11

US-08-974-549A-343

; Sequence 343, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

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; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

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; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026100S
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; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56...3454
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
; US-08-974-549A-343

Alignment Scores:

Pred. No.: 0 Length: 4037
Score: 6048.00 Matches: 1148
Percent Similarity: 99.91% Conservative: 1
Best Local Similarity: 99.83% Mismatches: 1
Query Match: 99.49% Indels: 0
DB: 3 Gaps: 0

US-08-951-733-20 (1-1154) x US-08-974-549A-343 (1-4037)

Qy 5 GlnArgCysValLeuLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
Db 2 CAGCGTCGCTCTGCTGCGCACGCTGGGAGCCCTGGCCGCCACCCCGCGATGCG 61
Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTGCGGAGCGCTGCGTCCCTGTGCGCACCCACTACCCGAGGTGCTG 121
Qy 45 ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGCTGGCCAGCTTCGTGCGGCGCTGGGGCCCGCAGGCTGGCGGTGGTGGTGGCGGG 181
Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCCGGCGGCTTTCCGCGCGCTGTGTGCGCCAGTGCCTGGTGTGCTGCCCTGGAGCA 241
Qy 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCGCGCGCGCGCGCGCTCCCTCGCGAGGTGTCCCTGCTGAAAGAGCTGGTGCC 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAGAACGCTGTGGCTTCGGCTTCGCG 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGACGGGGCGCGGGGGCGCGCGCGCGCGCGCGCTTACACACAGCGTGCAGCTAC 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrPglyLeuLeuLeuArg 164

| | | | |
|----|------|---|------|
| Db | 422 | CTGCCCAACAGGTGACGACGACACTGCGGGGAGCGGGCGTGGGGCTGCTGCTGCCG | 481 |
| QY | 165 | ArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal | 184 |
| Db | 482 | CGCGTGGGCGACAGCTGTGTTACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTG | 541 |
| QY | 185 | AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr | 204 |
| Db | 542 | GCTCCACAGTGCCTTACCAGGTGTGCGGGCCCGCTGTACCAGCTGCGCGCTGCCACT | 601 |
| QY | 205 | GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla | 224 |
| Db | 602 | CAGGCCCGCCCCCGCACAGCTAGTGACCCCGAAGCGCTCTGGATGCGAAGGGCC | 661 |
| QY | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| Db | 662 | TGGAAACATAGCGTCAAGGAGGCGGGGTCCCGCTGGGCTGCAGCCCGGGTGGGAG | 721 |
| QY | 245 | ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla | 264 |
| Db | 722 | AGGCGGGGGGAGTCCAGCGGAAGTCTGCCGTTCGCCAAGAGGCCAGCGGTGGCGCT | 781 |
| QY | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| Db | 782 | GCCTCTGAGCGGAGCGGACGCCGCTTGGCAGGGTCTCTGGGCCACCACCGGSCAGGAC | 841 |
| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| Db | 842 | CGTGGACCGAGTACCGGTGTTCTGTGTGGTGTACCTGCCAGACCCCGCCGAAGAGCC | 901 |
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| Db | 902 | ACCTCTTTGGAGGTGCGCTCTCTGGCAGCGGCCACTCCACCACATCCGTGGGCGGCCAG | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| Db | 962 | CACCAGCGGGCCCGCCATCCACATCGCGGCCACCACGCTCCCTGGGACACGCCCTTGCTCC | 1021 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| Db | 1022 | CGGGTACCGCGAGACCAAGCACTTCCCTCTACTCTCAGCGCACCAAGGAGAGCTGCGG | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| Db | 1082 | CCCTCCTTCTACTAGCTCTCTGAGGCCAGCGCTGCTGCGCTCGGAGGCTCTGTGGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| Db | 1142 | ACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCGCAGGTTGCCCCCGCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCCAGCGGTACTGGCAATGGCGGCCCTCTTCTGGAGCTGCTGGGAACCAACGCGCAG | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCCACGGGTGTCTCTCAAGACGCACTGCCCGCTCGAGCTGCGGTCAACCCAGCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| Db | 1322 | GC CGGTGTCTGTGCCCGGAGAGGCCCGCAGGGCTCTGTGGCGGCCCGCCGAGGAGGAC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| Db | 1382 | ACAGACCCCGCTGCTGTGTGACGTGCTCCCGCAGCACAGACGCCCTGGCAGGTGTAC | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| Db | 1442 | GGGTTCTGGGGCTTGCTTGGCCCGCTGGTGGCCCGCAGGCCCTCTGGGGCTCAGGAC | 1501 |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 |
| Db | 1502 | AACGAACGCCGCTTCTCAGGAACACCAAGAGTTCTATCTCCCTGGGGAAGCATGCCAAG | 1561 |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 |
| Db | 1562 | CTCTCGCTGACGAGAGTGCAGTGGAAAGATGAGCTGCGGACTGCGCTTGGCTGCGCAGG | 1621 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla | 564 |
| Db | 1622 | AGCCCAAGGGTGTGCTGTGTTCGGCCGACAGACCGTCTGCGTGAAGAGATCCTGGCC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr | 584 |
| Db | 1682 | AGTTCTCTGACCTGGCTGATGAGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTAT | 1741 |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| Db | 1742 | GTCAACGAGACCACTGTTCAAAAGAACAGGCTCTTTTCTACCGCGCAGTGTCTGAGC | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuLeuGluLeuSer | 624 |
| Db | 1802 | AGTTGCAAGCATTTGGATTCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGCG | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| Db | 1862 | GAAGCAGAGGTCAAGCAGCATTCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| Db | 1922 | TTCATCCCCAAGCTGACGGGCTGCGGCCGATTTGTGAACATGGCACTACGTCGTGGGAGCC | 1981 |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| Db | 1982 | AGAACGTTCCGCAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAGGCACTGTTTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
| Db | 2042 | AGCGTGTCAACTACGAGCGGGCGGCGCGCGCTCTCTGGCGCTCTGTGCTGGGC | 2101 |
| QY | 705 | LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro | 724 |
| Db | 2102 | CTGGAGATATCCACAGGGCTGCGGCACCTTCGTGCTGTGCGGGCCGACGAGCCCG | 2161 |
| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 |
| Db | 2162 | CCGCTTGAGCTGTACTTGTCAAGTGGATGTGACGGCGCGCTACGACACATCCCCCAG | 2221 |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleLysProGlnAsnThrTyrCysValArg | 764 |
| Db | 2222 | GACAGGCTCACGGAGGTCTCGCCAGCATCATCAACCCCGAAGACAGTACTGCGTGGT | 2281 |
| QY | 765 | ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
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| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 |
| Db | 2342 | GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGAG | 2401 |
| QY | 805 | ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 |
| Db | 2402 | ACCAGCCCGCTGAGGGATGCCGTCTCATGACGAGAGCTCCTCCCTGAATGAGGCCAGC | 2461 |
| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly | 844 |
| Db | 2462 | AGTGGCTCTTTCACGCTTCTTCCGTTCATGTGCCACACCGCGCTGCGCATCAGGGGC | 2521 |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| Db | 2522 | AACTCTACGTCCAGTCCAGGGATCCCGAGGGCTCCATCTCTCTCCAGCTGCTCTGC | 2581 |
| QY | 865 | SerLeuCystyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 |
| Db | 2582 | AGCTGTGCTACGGCAGATGGAGAACAGCTGTTTGGGGGATTCGGCGGAGCGGCTG | 2641 |

QY 885 LeuLeuArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
DB 2642 CTCCTGCGTTGGTGAGATTCCTGTGTGGTACACCTCACCTCACCCACGCGAAACCC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
DB 2702 TTCCTCAGGACCTGTGTCGAGGTCTCCTGAGTATGCTGCGTGTGAACCTGCGGAG 2761
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
DB 2762 ACAGTGTGTAACTTCCCTGTAGAGACGAGGCGCTGCGTGGCAGCGCTTTGTTCAGATG 2821
QY 945 ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuLeuAspThrArgThrLeuGluVal 964
DB 2822 CCGGCCACGCGCTATTCCTGTCGCGCTGCTGCTGGATACCCGAGCCCTGGAGGTG 2881
QY 965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984
DB 2882 CAGAGCGACTACTCCAGCTATGCCGCGACCTCCATCAGAGCCAGTGTACCTTCAACCGC 2941
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DB 2942 GGCTTCAAGGCTGGGAGAACATCGTGCAGAACTCTTTGGGGTCTTTCGGCTGAAGTGT 3001
QY 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
DB 3002 CACAGCGTGTTCCTGAGTTCAGAGTGCAGACGCTCCAGACGGTGTGACCAACATCTAC 3061
QY 1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
DB 3062 AAGATCCTCCTGCTGCAGCGCTACAGGTTTTCACGCATGTGTGTCAGCTCCCATTTTCAT 3121
QY 1045 GlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
DB 3122 CAGCAAGTTTGAAGAAGACCCACATTTTCTGCGCGTCTCTCTGACACGCGCTCCCTC 3181
QY 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
DB 3182 TGCTACTCCATCTCCGAAGCAAGCAAGCAGGATGTCGTGGGGGCCAAGGGCGCGCC 3241
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DB 3242 GGCCCTCTGCCCTCCGAGCGCGTGCAGTGGTGTGCCACCAAGCATCTCTCTCAAGCTG 3301
QY 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
DB 3302 ACTCGACACCGTGTACCTAGTCCACTCCTGCGGGTCACTCAGGACAGCCAGACGCGAG 3361
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RESULT 12

US-08-974-549A-638
; Sequence 638, Application US/08974549A
; Patent No. 6166178

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; APPLICANT: Lingner, Joachim
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; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

/note= "http-encoding sequence employing
alternative codon distributions for
E. coli (all genes)"
US-08-974-549A-638

Alignment Scores:

Pred. No.: 0
Score: 5961.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 98.06%
DB: 3
Length: 3396
Matches: 1132
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-08-951-733-20 (1-1154) x US-08-974-549A-638 (1-3396)

QY 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42
Db 1 ATGCCCGCGCGCGCGCTGCCGCGGTGCCAGCTGCTGCAGCATTTATCCGAA 60
QY 43 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 62
Db 61 GTGCTCCGCTGGCAGACTTTGTGCGCCGCTGGGCCCGCAGGGCTGGCGCTGGTGAC 120
QY 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 82
Db 121 CGCGCGATCCGCGCGCTTCCGCGCTGGTGCGCAGTGCCTGCTGGTGGCGCTGG 180
QY 83 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
Db 181 GATGCCGCGCGCGCGCGCGCGAGCTTTCCGCAGGTGAGCTGCCTGAAAGAACTG 240
QY 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 122
Db 241 GTGGCGCGGTGCTGCAGCGCTGTGCGAACCGCGCGCGCGCGCGCTGGCTTTGGC 300
QY 123 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 142
Db 301 TTTCGCTGCTGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 143 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrPglyLeuLeu 162
Db 361 AGTATCTCCGAACACCGTGAACGATGCGCTGCGCGCAGCGCGCGCTGGGCGTCTG 420
QY 163 LeuArgArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 182
Db 421 CTGGCGCGGTGGCGCATGATGTGCTGTGTCATCTGCTGGCGCGCTGCGCGCTTTGTG 480
QY 183 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 202
Db 481 CTGGTGGCGCGAGCTGCGGTATCAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 203 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 222
Db 541 GCGACCCGCGCGCGCGCGCGCATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 223 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 242
Db 601 CGCGCTGGAACCATAGCTGCGCGAAGCGCGCTGCGCTGCGCGCGCGCGCGCGCG 660
QY 243 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 262
Db 661 GCGCGCGCGCGCGCGCGAGCGAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 263 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 282
Db 721 GCGCGCGCGCGCGAAGCGACCGCGGTGGCGCAGCGCAGCTGGCGCGCATCCGGCG 780
QY 283 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 302
Db 781 CGACCCGCGCGCGCGAGCATCGCGCTTTGCGTGGTGGCGCAGCGCAGCTGGCGCATCCGGCG 840
QY 303 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 322
Db 841 GAAGCAGCAGCCTGGAAGCGCGCTGAGCGCACCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 323 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 342
Db 901 CGCCAGCATCATCGCGCGCGCGCGCAGCACCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 343 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 362
Db 961 TCGCCCGCGGTATTCGGAACCAACATTTCTGTATAGCAGCGCGCGCGCGCGCGCGCG 1020
QY 363 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 382
Db 1021 CTGGCGCGCGAGCTTTCTGCTGAGCAGCTTGCGCCCGAGCGCTGACCGCGCGCGCGCTG 1080

QY 383 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 402
Db 1081 GTGGAACCATTTTCTGGSCAGCCCGCTGGATCGCGGACCCCGCGCGCTGCCG 1140
QY 403 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 422
Db 1141 CGCTGCCGCGAGCTATTGGCAGATGGCGCGCTGTTCTGGAATCTGCTGGCAACCAT 1200
QY 423 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 442
Db 1201 GCGACGTGCCGCTATGGCTGCTGCTGAAAACCATTTGCCGCTGCGCGCGCGTACC 1260
QY 443 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 462
Db 1261 CGCGCGCGCGCGCTGTCGCGCGCGAAACCCAGCGGCGAGCTGCGCGCGCGGAAGA 1320
QY 463 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 482
Db 1321 GAAGATACCATTCGCGCGCGCTGTGTCAGCTGCTGCGCAGCATAGCAGCGCTGGCAG 1380
QY 483 ValTyrGlyPheValArgAlaCysLeuArgLeuValProProGlyLeuTyrGlySer 502
Db 1381 GTGATGGCTTTGTCGCGCTGCTGCGCGCTGCTGCGCGCGCGCGCTGCGCGCAGC 1440
QY 503 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 522
Db 1441 CGCCATTAACGAACCGCGCTTCTGCGCAACACCAAAAAATTTATTAGCCTGGCAACAT 1500
QY 523 AlaLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTyrLeu 542
Db 1501 GCGAACTGAGCTGCGAGNACTGACCTGGAAAATGAGCGTGGCGGCTGCGCGTGGCTG 1560
QY 543 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIle 562
Db 1561 CGCGCAGCGCGCGCTGGCTGCTGCGCGCGCGGCAACATCGCTGCGCGAAGAAAT 1620
QY 563 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 582
Db 1621 CTGGCGAAATTTCTGCTATGGCTGATGAGCGTATGTGGTGAACCTGCTGCGCAGCTTT 1680
QY 583 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 602
Db 1681 TTTTATGTACCCGAAACCCACTTTCAGAAAAACCGCTGTTTTTTATCCAAAGCGTG 1740
QY 603 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 622
Db 1741 TGGAGCAACTGCAGAGCATTTGCCATTCGCCACCATCTGAAACGCGTGCAGCTGCGGAA 1800
QY 623 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 642
Db 1801 CTGAGCGAAGCGGAGTGGCGCAGCATCGCAAGCGCGCGCGCGCTGCTGACGCGCGC 1860
QY 643 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 662
Db 1861 CTGCGCTTTATCCGAAACCGGATGGCTGCGCGCGATTTGTAACATGGATTATGGTG 1920
QY 663 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 682
Db 1921 GCGCGCGCACCTTTTCGCGCGGAAACCGCGGGAACGCTGACCGCGCGCTGGAAGCG 1980
QY 683 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 702
Db 1981 CTGTTTAGCTGTGAACATATGAACGCGCGCGCGCGCGCTGCTGGCGCGAGCGTG 2040
QY 703 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 722
Db 2041 CTGGCGCTGGATGATATTATCGCGCTGGCGCACCTTTGTGTCGCTGCGCGCGCAG 2100
QY 723 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 742
Db 2101 GATCCCGCGCGGAACTGTATTTTGTGAAGTGGATGTGACCGCGCGCTGATGATACCAT 2160

QY 743 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 762
DB CCGCAGGATCGCTGACCGAAGTATTCGAGCATATTATAACCGCAGAACACCTATTGC 2220
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DB GTGCGCCCTATGCGGTGGTGCAGAAAGCGCGATGGCCATGTGCGCAAGCGCTTTAA 2280
QY 783 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 802
DB AGCCATGTGAGCACCCCTGACCGATCTGCAGCGTATATGCGCCAGTTGTGCGCATCTG 2340
QY 803 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGlu 822
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QY 843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 862
DB CGCGCAAAAGCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 863 LeuCysSerLeuCysTyrGlyAspMetGlnLysLeuPheAlaGlyIleArgArgAsp 882
DB CTGTGCGACCTGTGTATGCGGATATGGAACAACTGTGTGCGGCGATTCGCGCGAT 2580
QY 883 GlyLeuLeuLeuArgLeuValAspPheLeuValThrProHisLeuThrHisAla 902
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QY 903 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 922
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QY 923 ArgLysThrValValAsnPheProValGlnAspGluAlaLeuGlyGlyThrAlaPheVal 942
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QY 983 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 1002
DB AACCGCGCTTTAAAGCGCGCGCAACATGCGCGCAACTGTGCTGCTGCTGCTGCTGCTG 2940
QY 1003 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1022
DB AAATGCCATAGCTTTCTGGATCTGAGTGAACGCTGACGCTGACGCTGCTGCTGCTGCTG 3000
QY 1023 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1042
DB ATTTATAAATTCGCTGCTGCGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
QY 1043 PheHisGlnGlnValThrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1062
DB TTTTCATCAGCAGGTGTGAAACCCGACCTTTTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 3120
QY 1063 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
DB AGCTGTGCTATAGCATCTGAAAGCGAAACCGCGGCGATGAGCCCTGGCGCGCAAGGC 3180
QY 1083 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1102
DB CGCGCGCGCGCTGCGCGAGGAGCGTGCAGTGGCTGCTGCCATCAGCGCTTCTGCTGCTG 3240
QY 1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122

DB 3241 AAACCTGACCGCATCGCTGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
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DB ACCCAGCTGACCGCAAACTGCGGCGCACCACTGACCGCTGACCGCTGGAAGCGCGCGAAC 3360
QY 1143 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1154
DB CCGCGCTGCGCGAGCGATTTTAAACCACTTCTGGAT 3396
RESULT 13
US-08-974-549A-639
; Sequence 639, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted

QY 603 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 622
DB 1741 TGGTCCAACCTGCGAGTCATCGGTATCGGTGAGCAACCTGGAACCGTTGTCAGCTGCGTGAA 1800
QY 623 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 642
DB 1801 CTGTCCGAAGCTGAAGTTCTGTCAGCACCGTGAAGCTGTCGGGTCTGCTGACCTCCCGT 1860
QY 643 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 662
DB 1861 CTGGCTTTTCATCCGAAACCGAGCGTCTGGCTCCGATCGTTAACTGAGCTACGTTGTT 1920
QY 663 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 682
DB 1921 GGTGCTGCTACTTCCGTCGCGTGAAGAAACGCTGCTGAACGCTCTGACCTCCCGTGTAAAGCT 1980
QY 683 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuGlyAlaSerVal 702
DB 1981 CTGTTCTCCGTTCTGAACCTAGAACGTCGTCGTCGGGTCTGCTGGGTGCTTCCGTT 2040
QY 703 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 722
DB 2041 CTGGTCTGGACGACATCCACCGTGTGGCGTACCTTCGTTCTGCGTGTGCTGCTCAG 2100
QY 723 AspProProGluLeuLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 742
DB 2101 GACCGCGCGCGGAACCTGATCTGCTTAAAGTTGACGTTACCGGTGCTTACGACACCATC 2160
QY 743 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 762
DB 2161 CCGCAGGACCGTCTGACCGAAGTTATCGTTCATATCATCAACCGCAGAACCTACTGCG 2220
QY 763 ValArgArgTyrAlaValAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 782
DB 2221 GTTCGTCGTTACGCTGTGTTTCAGAAAGCTGCTCACGTCACGTTCTGTAAGCTTTCAA 2280
QY 783 SerHisValSerThrLeuThrAspGlnProTyrMetArgGlnPheValAlaHisLeu 802
DB 2281 TCCACAGCTTCCACCCCTGACCGACTGCAGCCGTACATGCGGTACAGTTCGTTGCTGCACCTG 2340
QY 803 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAspGlu 822
DB 2341 CAGGAAACCTCCCGCGCTGCGTAGCGCTGTGTTATCGAAGACGTCCTCTCCCTCGAAGAA 2400
QY 823 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 842
DB 2401 GCTTCCCTCCGGTCTGTTCGACGTTTCTGCGTTTCATGTGCCACACGCTGTTGCTGATC 2460
QY 843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 862
DB 2461 CGTGGTAAATCTCTACGTTCAAGTCCAGGGTATCCCGCAGGGTTCCATCTGTCCACCGCTG 2520
QY 863 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 882
DB 2521 CTGTGCTCCCTGCTGCTACGCTGACATGGAACAAACTGTTCGCTGATCCCGTCGTCGAC 2580
QY 883 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 902
DB 2581 GGTCTGCTGCTGCTGCTGTTGACGACTTCTGCTGCTGTTACCCGCGACCTGACCCACGCT 2640
QY 903 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 922
DB 2641 AAAACCTTCTCGGTACCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
QY 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942
DB 2701 CGTAAACCGTGTGTTAACTTCCCGGTTGAAGACGAGCTCTGGGTGATACCGCTTTCGTT 2760
QY 943 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 962
DB 2761 CAGATGCCGCTCACGCTCTGTTCCCGTGTGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820

QY 963 GluValGlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 982
DB 2821 GAAGTTCAAGTCGACTACTCTCTACGCTCGTACTCCATCCGTCGCTTCCCTGACCTTC 2880
QY 983 AsnArgGlyPheLysAlaGlyArgAsnMetArgLysLeuPheGlyValLeuArgLeu 1002
DB 2881 AACCGTGGTTTCAAAGCTGGTCGTAACATGCGTCGTAAACATGTTCTGCGTGTCTGCGCTG 2940
QY 1003 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1022
DB 2941 AAATGCCACTCCCTGCTTCTGGACCTGCAGGTAACTCCCTGCAGACCGTTTGCACCAAC 3000
QY 1023 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1042
DB 3001 ATCTACAAATCTGCTGCTGACGCTTACCGTTTCCACGCTTGGCTTCTGACGCTGCG 3060
QY 1043 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1062
DB 3061 TTCACCAAGCAGGTTTGGAAACCCGACCTTCTTCTGCTGCTGTTATCTCCGACACCGCT 3120
QY 1063 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
DB 3121 TCCCTGTGCTACTCCATCTCGAAGCTTAAACCGCTGATGTCCTCGGTGCTTAAAGT 3180
QY 1083 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1102
DB 3181 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
QY 1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122
DB 3241 AAATGACCCGCTACCGGTGTTACCTAGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
QY 1123 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1142
DB 3301 ACCCAGCTGTCCTGTAACCTCCCGGTACCACTGACCGCTGACCGCTGCGAAGCTGCTGCTAAC 3360
QY 1143 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1154
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RESULT 14
US-08-974-549A-640
; Sequence 640, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

;; PRIOR APPLICATION DATA: US 08/844,419
;; FILING DATE: 18-APR-1997
;; PRIOR APPLICATION DATA: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIOR APPLICATION DATA: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIOR APPLICATION DATA: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; PRIOR APPLICATION DATA: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 640:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3396 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..3396
;; OTHER INFORMATION: /note= "HTRT-encoding sequence employing
;; OTHER INFORMATION: alternative codon distributions for
;; OTHER INFORMATION: yeast (all genes)"
US-08-974-549A-640

Alignment Scores:

| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 0 | Length: | 3396 |
| Score: | 5961.00 | Matches: | 1132 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 98.06% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-08-951-733-20 (1-1154) x US-08-974-549A-640 (1-3396)

| | | | |
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| QY | 23 | MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu | 42 |
| DB | 1 | ATGCCAAGAGCTCCAGATGTAGAGCTGTAGATCTTTGTTGAGATCTCATTTATAGAGAA | 60 |
| QY | 43 | ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln | 62 |
| DB | 61 | GTTTTGCCATTGGCTACTTTTCTTAGAAGATTGGGTCCACAGGTTGGAGATTGGTTCAA | 120 |
| QY | 63 | ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp | 82 |
| DB | 121 | AGAGGTGATCCAGCTGCTTTTGTAGAGCTTTGGTTGCTCAATGTTGGTTGTTCATGG | 180 |
| QY | 83 | AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu | 102 |
| DB | | | |

| | | | |
|-----|--|---|------|
| 181 | GATGCTAGACCACCACAGCTGCTCCATCTTTTAGACAAGTTTCTTGTGTTGAAGAAATG | 240 | |
| 103 | ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLeuAsnValLeuAlaPheGly | 122 | |
| DB | 241 | GTGCTAGAGTTTTCAAAAGATTGTGTGAAGAGGTGCTAAAAATGTTTGGCTTTGGT | 300 |
| QY | 123 | PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg | 142 |
| DB | 301 | TTTGCTTTGTTGGATGGTCTAGAGGTGGTCCACAGAAGCTTTTACTACTTCTGTGTAGA | 360 |
| QY | 143 | SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu | 162 |
| DB | 361 | TCTTATTTGCCAAATACTGCTTACTGATGCTTTGAGAGGTCTGGTCTTGGGTTGTG | 420 |
| QY | 163 | LeuArgArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal | 182 |
| DB | 421 | TTGAGAAGAGTTGGTGATGATGTTTGGTTTCATTTTGGCTAGATGCTGTTTGTGTT | 480 |
| QY | 183 | LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla | 202 |
| DB | 481 | TTGGTTGCTCCATCTTGTGCTTATCAAGTTTGGTCCACCATTTGATCAATTTGGTGT | 540 |
| QY | 203 | AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu | 222 |
| DB | 541 | GCTACTCAAGCTAGACCACCACCATGCTTCTGGTCCAAGAAGAGATTGGTCTGAA | 600 |
| QY | 223 | ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 242 |
| DB | 601 | AGAGCTTGGAAATCTCTGTTAGAGAAGCTGGTGTCCATTTGGGTTGGCAGCTCCAGT | 660 |
| QY | 243 | AlaArgArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 262 |
| DB | 661 | GCTAGAAGAAGAGGTGGTCTGCTCTAGATCTTTGCCATTTGCCAATAAGACCAAGA | 720 |
| QY | 263 | GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 282 |
| DB | 721 | GGTGTGCTCCAGACCAAGAACTCCAGTTGGTCAAGGTTCTTGGGCTCATCCAGGT | 780 |
| QY | 283 | ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu | 302 |
| DB | 781 | AGAACTAGAGGTCCATCTGATAGAGGTTTTTGTGTTGTTTCTCCAGCTAGACCAGTGA | 840 |
| QY | 303 | GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 322 |
| DB | 841 | GAAGTACTTCTTTGGAAGGTGCTTGTCTGGTACTAGACATTTCTCATCTCTGTGTGT | 900 |
| QY | 323 | ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro | 342 |
| DB | 901 | AGACAACATCATGCTGGTCCACCATCTACTTCTAGACCAACCAAGACCATGGGATATCCA | 960 |
| QY | 343 | CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln | 362 |
| DB | 961 | TGTCCACCAAGTTTATGCTGAAATAAACATTTTTTGTATTCTTCTGCTGATAAAGAACA | 1020 |
| QY | 363 | LeuArgProSerPheLeuLeuSerSerLeuArgProProSerLeuThrGlyAlaArgLeu | 382 |
| DB | 1021 | TTGAGACCATCTTTTGTGTTGCTCTTTGAGACCATCTTTGACTGCTGCTAGAAATG | 1080 |
| QY | 383 | ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro | 402 |
| DB | 1081 | GTGTGAACATTTTTTTTGGGTTCTAGACCATGGATGCCAGGTACTCCAGAGAGATTGCCA | 1140 |
| QY | 403 | ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis | 422 |
| DB | 1141 | AGATTGCCACAAGATATTTGGCAATGAGACCATTTCTTTTGGAAATTTGTTGGGTAATCAT | 1300 |
| QY | 423 | AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr | 442 |
| DB | 1201 | GCTCAATGTCCATATGTTGTTTGTGTAATAACTCATTTGCTCATTTGAGAGCTGCTGTACT | 1260 |
| QY | 443 | ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu | 462 |
| DB | 1261 | CCAGCTGCTGGTGTGTTGCTAGAGAAACCAACCAAGGTTCTGTTGCTGCTCCAGAAAGA | 1320 |

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QY 463 GluAspThrAspProArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 482
Db 1321 GAAATACTGATCCAAAGAAGATTGGTTCAATTTGTAGACAAACATCTCTCCATGGCAA 1380
QY 483 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 502
Db 1381 GTTATATGGTTTGTAGAGCTTGTGTGAGAAAGATTGGTCCACAGGTTTGTGGGGTCT 1440
QY 503 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHis 522
Db 1441 AGACATATGAAGAAGATTTTTCAGAAATACATAAAAAATTATTTCTTTGGGTAAACAT 1500
QY 523 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 542
Db 1501 GCTAAATGTCTTTTCCAAAGATTCACCTGGAAAAATGCTGTGTAGAGATTGTGCTGGTTG 1560
QY 543 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 562
Db 1561 AGAAGATCTCCAGGTGTGGTGTGTCCAGCTGCTGAACATAGATTGAGAGAAAGAAAT 1620
QY 563 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 582
Db 1621 TTGGCTAAATTTTTCGATTTGCTGATCTGCTTTATGTTGTGAATTTGTGAGATCTTTT 1680
QY 583 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 602
Db 1681 TTTTATGTTACTGAACACTCTTTTCAAAAAATAGATTGTTTTTTTATAGAAAACTGTT 1740
QY 603 TrpSerLysLeuGlnSerIleGlyLeuArgGlnHisLeuLysArgValGlnLeuArgGlu 622
Db 1741 TGGTCTAAATTTGCAATCTATTGGTATTAGACACACTTTGAAGAGTTCAATTGAGAGAA 1800
QY 623 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 642
Db 1801 TTGTCTGAAGCTGAAGTTAGACAACTAGAGAACCTAGACAGCTTTGTGACTTCTAGA 1860
QY 643 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 662
Db 1861 TTGAGATTTATTTCCAAAACCAAGATGGTTTGGAGACCAATGTTTAATATGGATTATGTTG 1920
QY 663 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 682
Db 1921 GGTCTAGAACTTTTAGAGAGAAAAAGAGCTGAAGAGATTGACTTCTAGAGTTAAAGCT 1980
QY 683 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 702
Db 1981 TTGTTTCTGTTTGTGAATTTATGAAGAGCTAGAGACCAAGCTTTGTTGGTGTCTGTT 2040
QY 703 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 722
Db 2041 TTGGGTTTGGATGATATTCATAGAGCTTGGAGAACTTTTCTTTTGAGAGTTAGAGCTCAA 2100
QY 723 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 742
Db 2101 GATCCACCACCAGANTTGTATTTGTAAAGTTGAGTTACTGGTGCTTATGATACATT 2160
QY 743 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 762
Db 2161 CCACAGATAGATTGACTGAAGTTATTGCTTCTATTATTAACACACAAAATACTATTGT 2220
QY 763 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 782
Db 2221 GTTAGAAGATATGCTGTGTGTTCAAAAGCTGCTCATGGTCTATGTAGAAAAGCTTTTAAA 2280
QY 783 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 802
Db 2281 TCTCATCTTCTACTTTGACTGATTTCGAACCATATATAGACAAATTTGTGCTCATTTG 2340
QY 803 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu 822
Db 2341 CAAGAAACTTCTCCATTGAGAGATGCTGTGTTATTGAAACAACTTCTTCTTTGGAATGAA 2400
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RESULT 15

US-08-974-549A-641

; Sequence 641, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

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QY 823 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 842
Db 2401 CTTCTCTGCTGTTGTTGATGTTTTTTTGTAGATTTATGTGTCATCATGCTGTTAGAATT 2460
QY 843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlnSerIleLeuSerThrLeu 862
Db 2461 AGAGGTAAATCTTATGTGTCAATGTCAAGGTATCCACAAGGTTCTATTTTCTCTACTTTG 2520
QY 863 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 882
Db 2521 TTGTGTTCTTGTGTTATGTTGATATGGAATAAATTAATTTGTTGCTGTTATAGAGAGAT 2580
QY 883 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 902
Db 2581 GGTTTGTTGTTGAGATTGGTTGATGATTTTTTTTGTGTTACTCCACATTTGACTCATGCT 2640
QY 903 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 922
Db 2641 AAAAATTTTTTGAAGACTTTTGGTTAGAGGTGTTCCAGAAATATGTTGTGTTGTTAAATTTG 2700
QY 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942
Db 2701 AGAAAACTGTGTTTAATTTTCCAGTTGAAGATGAAGCTTTGGGTGGTACTGCTTTGTT 2760
QY 943 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 962
Db 2761 CAAATGCCAGCTCATGTTTCTTCCATGGTGTGTTTGTGTTGTTGGATACTAGAATTTG 2820
QY 963 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 982
Db 2821 GAACTTCAATCTGATTAATCTTCTTATGCTAGAATCTCTATTAGAGCTTCTTTGACTTTT 2880
QY 983 AsnArgGlyPheLysAlaGlyArgAsnMetArgLysLeuPheGlyValLeuArgLeu 1002
Db 2881 AATAGAGGTTTAAAGCTGTAGAAATATAGAGAGAAATTTGTTGGTGTTCAGATTG 2940
QY 1003 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1022
Db 2941 AAATGTCATCTCTTGTGTTTGGATTTGCAAGTTAATCTTTGCAAACTGTTTGTACTAAT 3000
QY 1023 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1042
Db 3001 ATTTATAAATTTTGTGTGCAAGCTTATAGATTTCATGCTTGTGTTTTCGAATTTGCCA 3060
QY 1043 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1062
Db 3061 TTTTCATCAACAAGTTTGGAAAAATCCAACTTTTTTTTTTGACAGTTATTTCTGATACTGCT 3120
QY 1063 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
Db 3121 TCTTTGTGTTATTCTATTATTTGAAAGCTAAAAATGCTGTTATGCTTTGGGTGCTAAAGGT 3180
QY 1083 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1102
Db 3181 GCTGCTGGTCCATTGCCATCTGAAGCTGTTCAAATGGTGTGTCATCAAGCTTTTTTGTG 3240
QY 1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122
Db 3241 AAATTTGACTAGACATAGAGTTTACTTATGTTCCATTTGTTGGTCTTCTTTGAGAACTGCTCAA 3300
QY 1123 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1142
Db 3301 ACTCAATTTGCTAGAAAAATTCAGAGTACTACTTTGACTGCTGTTTGGAGGCTGCTTAAT 3360
QY 1143 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1154
Db 3361 CCAGCTTGGCACTGATTTTAAACATATTTTTGGAT 3396
```

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APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 641:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note= "HTRT-encoding sequence employing

OTHER INFORMATION: alternative codon distributions for
OTHER INFORMATION: yeast (high expressing genes)"
US-08-974-549A-641

Alignment Scores:

| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 0 | Length: | 3396 |
| Score: | 5961.00 | Matches: | 1132 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 98.06% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-08-951-733-20 (1-1154) x US-08-974-549A-641 (1-3396)

| | | | |
|----|-----|--|-----|
| QY | 23 | MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu | 42 |
| Db | 1 | ATGCCAAGAGCTCCAAGATGTAGAGCTTTAGATCTTTGTTGAGATCTCACTACAGAGAA | 60 |
| QY | 43 | ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln | 62 |
| Db | 61 | GTITGGCCATTTGGCTACTTTTCGTTAGAAGATTGGGTCACAAAGATTGGAGATTGGTTCAA | 120 |
| QY | 63 | ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr | 82 |
| Db | 121 | AGAGGTGACCCAGCTGCTTTTCAGAGCTTTGGTTGCTCAATGTTGGTTGTTGTTCCATGG | 180 |
| QY | 83 | AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu | 102 |
| Db | 181 | GACGCTAGACCACCACGCTGCTCCATCTTTTCAGACAACTTTCTTTGTTTGAAGGAATTG | 240 |
| QY | 103 | ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysValLeuAlaPheGly | 122 |
| Db | 241 | GTTCGTAGAGTTTGGCAAGATTGTGTGAAGAGAGTGCTAAGAACGTTTGGTTCGCTT | 300 |
| QY | 123 | PheAlaLeuLeuAspGlyAlaArgGlyGlyProGlnAlaPheThrThrSerValArg | 142 |
| Db | 301 | TTGCGCTTTGTTGACGCTGCTAGAGTGCTCCACCAAGCTTTCTACTACTTCTGTAGA | 360 |
| QY | 143 | SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrPglyLeu | 162 |
| Db | 361 | TCCTACTTGCACAAACACTGTTACTGACGCTTTGAGAGGTTCTGGTGGTGGTGGTGGT | 420 |
| QY | 163 | LeuArgArgValGlyAspAspValLeuValHisLeuAlaArgCysAlaLeuPheVal | 182 |
| Db | 421 | TTGAGAAGAGTTGCTGACGAGCTTTTGGTTGCTTGTGGCTAGATGCTGTTGTTGCTT | 480 |
| QY | 183 | LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla | 202 |
| Db | 481 | TTGGTTGCTCCATCTTTGCTTACCAAGTTTGTGGTCCACCATTTGTACCAATTGGGTGCT | 540 |
| QY | 203 | AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGlu | 222 |
| Db | 541 | GCTACTCAAGCTAGACCACCACACGCTTCTGGTCCAAAGAAGAAGATTGGGTGTGAA | 600 |
| QY | 223 | ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 242 |
| Db | 601 | AGAGCTTGGAAACCACTCTGTTAGAGAAGCTGGTGGTTCATTTGGGTTGGCAGTCCAGGT | 660 |
| QY | 243 | AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 262 |
| Db | 661 | GCTAGAAGAAGAGGTGGTCTGCTTCTAGATCTTTGCCATTTGCCAAGAGACCAAGAGA | 720 |
| QY | 263 | GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 282 |
| Db | 721 | GGTGTCTGCTCCAGAACAGAAAGAACTCCAGTTGGTCAAGTTGCTTTGGGCTCACCAGGT | 780 |
| QY | 283 | ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu | 302 |
| Db | 781 | AGAACTAGAGGTCCATCTGACAGAGGTTCTGTGTTGTTTCTCCAGCTAGACCAAGTAA | 840 |
| QY | 303 | GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 322 |
| Db | 841 | GAAGCTACTCTTTTGGNAGGTGCTTGTCTGTGGTACTAGACACTCTCACCCTCTGTGGT | 900 |

| | | | | | | | |
|----|------|---|------|----|------|---|------|
| QY | 323 | ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro | 342 | QY | 683 | LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal | 702 |
| DB | 901 | AGACAACACACCGCTGGTCCACCATTCTACTAGACCACCAAGACCATGGGACACTCCA | 960 | DB | 1981 | TTGTTCTCTGTTTGAACCTACGAAAGAGCTAGAACACAGGTTGTTGGTGCTCTCTT | 2040 |
| QY | 343 | CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln | 362 | QY | 703 | LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln | 722 |
| DB | 961 | TGTCACACAGTTTACGCTGAACCTAACACCTTCTGTACTCTCTGGTGACAAAGAACAA | 1020 | DB | 2041 | TTGGGTTTGGAGCATTCACAGAGCTTGGAGAACTTTCGTTTGGAGAGTTAGAGCTCAA | 2100 |
| QY | 363 | LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu | 382 | QY | 723 | AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle | 742 |
| DB | 1021 | TTGAGACCATCTTCTGTTGCTCTCTTTGAGACCATCTTTGACTGGTGCTAGAAAGATTG | 1080 | DB | 2101 | GACCCACACCAAGAAATGTACTTCGTTAAGGTGACGTTACTGGTGCTTAGACACTATT | 2160 |
| QY | 383 | ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro | 402 | QY | 743 | ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys | 762 |
| DB | 1081 | GTTCAAACTATTCTTGGGTTCTAGACCATTGGACGTTACTCCAAGAAGATTGCCA | 1140 | DB | 2161 | CCACAAGACAGATTGACTGAAGTTATTGCTTCTATTATTAAGCCACAAACACATTACTGT | 2220 |
| QY | 403 | ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis | 422 | QY | 763 | ValArgArgTyrAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLys | 782 |
| DB | 1141 | AGATTGCCACAAGATACTGGCAANTGAGACCATTTGTTCTTGGAAATTTGTTGGGTAACCA | 1200 | DB | 2221 | GTTAGAAGATACGCTGTTGTTCAAAGGCTGCTCACGGTCACGTTAGAAAGGCTTTCAG | 2280 |
| QY | 423 | AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr | 442 | QY | 783 | SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu | 802 |
| DB | 1201 | GCTCAATGTCCATACGCTGTTTGTGAAGCTCCTGTCATTGAGAGCTGCTGTACT | 1260 | DB | 2281 | TCTCACGTTCTACTTTGACTGACTTGCACCATACATGACAGCAATTCGTTGCTCATTG | 2340 |
| QY | 443 | ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu | 462 | QY | 803 | GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu | 822 |
| DB | 1261 | CCAGCTGCTGGTGTGCTGTAGAGAAAAGCCACAAGGTTCTGTTGCTGCCAGAAGAA | 1320 | DB | 2341 | CAAGAAACTTCTCCATTGAGAGAGCGTGTGTTATTGAACAATCTTCTCTTTGAACGA | 2400 |
| QY | 463 | GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln | 482 | QY | 823 | AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle | 842 |
| DB | 1321 | GNAGACACTGACCCAGAAGATTGGTTCAATGTTGAGACAACACTCTTCTCCATGGCAA | 1380 | DB | 2401 | GCTTCTTCTGTTGTTGCGACGTTTCTTGAGATTCATGTGTCCACGCGTTTAGAATT | 2460 |
| QY | 483 | ValTyrGlyPheValArgAlaCysLeuArgLeuValProProGlyLeuTrpGlySer | 502 | QY | 843 | ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu | 862 |
| DB | 1381 | GTTTACGTTTTCGTTAGAGCTGTTTTCGAAAGATTGTTCCACAGGTTGTTGGGGTCT | 1440 | DB | 2461 | AGAGTAAGTCTTACGTTCAATGTCAGGTATTCACAGGTTCTATTCTCTACTATTG | 2520 |
| QY | 503 | ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis | 522 | QY | 863 | LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp | 882 |
| DB | 1441 | AGACACAACGAAGAAGATTCTTGAGAAACACATAAGAAGTTCATTTCTTGGGTAAGCAC | 1500 | DB | 2521 | TTGTGTTCTTGTGTTACTCGGTGACATGGAAACAAGTTGTTGCGTGGTATTAGAAGAC | 2580 |
| QY | 523 | AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu | 542 | QY | 883 | GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla | 902 |
| DB | 1501 | GCTAAGTTGCTTTCGAAGAATTGACTTGGAAAGATGCTGTTAGAGACTGTGCTGGTTG | 1560 | DB | 2581 | GGTTTGTGTTGAGATTGGTTGACGACTTCTGTGTGGTTACTCCACACTTCGACTCAGCT | 2640 |
| QY | 543 | ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIle | 562 | QY | 903 | LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu | 922 |
| DB | 1561 | AGAAATCTCCAGGTGTTGTTGTTGCCAGCTGCTCAACACAGATTGAGAGAANAATT | 1620 | DB | 2641 | AAGACTTCTTGAGAACTTGTGTTAGAGGTGTTCCAGAAATACGCTGTGTTGTTAACTTG | 2700 |
| QY | 563 | LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe | 582 | QY | 923 | ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal | 942 |
| DB | 1621 | TTGGCTAAGTCTTGCACTGGTTGATGCTGTTTACGTTGTTGAATTTGTTGAGATCTTTC | 1680 | DB | 2701 | AGAAAGACTGTGTTTAACCTCCAGTTGAAGCAAGGCTTTGGGTGCTACTGCTTTCGTT | 2760 |
| QY | 583 | PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal | 602 | QY | 943 | GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu | 962 |
| DB | 1681 | TTCTACGTTACTGAACTACTTTCCAAAGAACACAGATTGTTCTTCTACAAAAGCTGTT | 1740 | DB | 2761 | CAAAATGCCAGCTCAGGTTGTTCCCATGGTGTGTTGTTGTTGGACACTAGAACCTTG | 2820 |
| QY | 603 | TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu | 622 | QY | 963 | GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe | 982 |
| DB | 1741 | TGGTCTAAGTTGCAATCTATTGGTATTATAGACACACTTTGAAGAGATTCAATTGAGAGAA | 1800 | DB | 2821 | GAAGTTCAACTCGACTACTCTTCTACGCTAGAACTTCTATTAGAGCTTCTTTGACTTTC | 2880 |
| QY | 623 | LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg | 642 | QY | 983 | AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu | 1002 |
| DB | 1801 | TTGTCTGAAGCTGAAGTTAGACAACACAGAGAAGCTAGACAGCTTTGTTGACTTCTAGA | 1860 | DB | 2881 | AACAGAGGTTTCAAGGCTGGTAGAAACATGAGAAAGAAAGTTGTTGCGTGTGTTGAGATTG | 2940 |
| QY | 643 | LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal | 662 | QY | 1003 | LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn | 1022 |
| DB | 1861 | TTGAGATTCAATCCAAAGCCAGACGGTTTGGAGACCAATTTGTAACATGGACTAGTTGTT | 1920 | DB | 2941 | AAGTGTCACTCTTTGTTCTTGGACTTGCAAGTTAACTCTTTTGGAAACTGTTTGTACTAAC | 3000 |
| QY | 663 | GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla | 682 | QY | 1023 | IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro | 1042 |
| DB | 1921 | GGTGCTAGAACTTTCAGAACGAAAGAGAGCTGAAGATTGACTTCTAGAGTTAAGGCT | 1980 | DB | 3001 | ATTTACAAGATTGTTGTTGTCGAAGCTTACAGATTCCACGCTGTGTTGTTGCAATTGCCA | 3060 |
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QY      ||||| 1083 AlaAlaGlyProLeuProSerGluAlaValGlnTTPLeuCysHisGlnAlaPheLeuLeu 1102
Db      ||||| 3181 GCTGTGGTCCATTGCCATCTGAAGCTGTCAATGGTTGTGCACCAAGCTTCTTGTGTG 3240
QY      ||||| 1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122
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QY      ||||| 1143 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1154
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GenCore version 5.1.6
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Title: US-08-951-733-14

Perfect score: 5018

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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 4996 | 99.6 | 4015 | 3 | US-08-854-050-224 |
| 4 | 4996 | 99.6 | 4015 | 4 | US-09-430-323-224 |
| 5 | 4996 | 99.6 | 4015 | 4 | US-09-572-423B-3 |
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| 11 | 4990 | 99.4 | 4037 | 3 | US-08-974-549A-343 |
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| 20 | 4614 | 91.9 | 4029 | 3 | US-08-851-843A-173 | Sequence 173, App |
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| 24 | 2885 | 57.5 | 51552 | 4 | US-09-733-294A-30 | Sequence 30, Appli |
| 25 | 2878 | 57.4 | 4200 | 4 | US-08-912-951-5 | Sequence 6, Appli |
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| 27 | 2878 | 57.4 | 15418 | 4 | US-09-783-203-1 | Sequence 1, Appli |
| 28 | 1618.5 | 32.3 | 2176 | 3 | US-08-974-549A-3 | Sequence 3, Appli |
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| 34 | 646 | 12.9 | 389 | 3 | US-08-851-843A-62 | Sequence 62, Appli |
| 35 | 646 | 12.9 | 389 | 3 | US-08-974-549A-8 | Sequence 8, Appli |
| 36 | 646 | 12.9 | 389 | 3 | US-08-854-050-62 | Sequence 62, Appli |
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| 39 | 406 | 8.1 | 3279 | 3 | US-08-851-843A-1 | Sequence 1, Appli |
| 40 | 406 | 8.1 | 3279 | 3 | US-08-974-549A-109 | Sequence 109, App |
| 41 | 406 | 8.1 | 3279 | 4 | US-08-854-050-1 | Sequence 1, Appli |
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ALIGNMENTS

RESULT 1

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; Sequence 224, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851.843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419

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; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
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; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:

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; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morlin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56...3454 /product= "htrr"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (htrr) catalytic protein
; OTHER INFORMATION: component"
US-08-854-050-224

Db 182 GACCCGGGGCTTTCCCGCGCGCTGGTGGCCAGTGCCCTGGTGTGCTGGCCCTGGAGCGCA 241
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Qy 185 AlaProSerCysAlaTrpGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
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Qy 205 GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla 224
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Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264
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Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
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Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluGluAla 304
Db 842 CGTGAGCCGAGTGACCGGTGTCTGTGTGGTGTCACTTCCACGACCGCGCGAAGAGCC 901
Qy 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324
Db 902 ACCTCTTGGAGGGTGGCTCTTGGCACGCGCCACTCCACCCATCCGTGGCGCGCCAG 961
Qy 325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344
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Qy 345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364
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Qy 365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384
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Qy 405 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln 424
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Db 1562 CTCTCGCTGAGGAGCTGAGCTGGAAGATGAGCGTGGGGACTCGCTTGGCTGCGCAGG 1621
Qy 545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla 564
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Qy 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
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Qy 645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664
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Db 2162 CCGCTCAGCTGTACTTTTTCAGGTGATGTGACGGGCGGTACGACACCATCCCCCAG 2221
Qy 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764
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Qy 765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
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QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
Db 2462 AGTGGCCTCTTCGACGCTCTCTACGCTTCATGTGCCACACCGCGTGGCATCAGGGGC 2521
QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
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QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
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QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
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Db 2702 TTCTCTAGAGACCTGGTCCGAGGTGTCCGTGATGCTGCTGGTGAACCTTGCAGAG 2761
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
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QY 945 ProAlaHisGlyLeu 949
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RESULT 5
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; Sequence 3, Application US/09572423B
; Patent No. 6331399
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William A. Gaarde
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0462
; CURRENT APPLICATION NUMBER: US/09/572,423B
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3454)
US-09-572-423B-3

Alignment Scores:
Pred. No.: 6,31e-264 Length: 4015
Score: 4996.00 Matches: 945
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.56% Indels: 0
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US-08-951-733-14 (1-949) x US-09-572-423B-3 (1-4015)

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QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTGGCAGCCGCTGCTCCCTGCTGCGCAGCAGCTACCGCAGGTGCTG 121
QY 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
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QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
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QY 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 194
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QY 205 GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
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QY 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
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QY 465 ThrAspProArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGlnValTyr 484
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Db 1442 GGCTTCGTGGGGCGCTGCTGCGCGGCTGTGTGCCCGCCAGGCTCTGGGGCTCCAGGCAC 1501
QY 505 AsnGluArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHisAlaLys 524
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Db 1562 CTCTCGCTGAGGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTCGGAGG 1621
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QY 605 LysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
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QY 665 ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
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QY 685 SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerValLeuGly 704
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QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
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QY 805 ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer 824
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QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
Db 2462 AGTGGCCCTTCTGACAGCTTCTCTAGCTTTCATGTGCCACCGCGGTGCGCATCAGGGGC 2521
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Db 2522 AAGTCTTACGTCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTGC 2581
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RESULT 6
US-09-128-354-1
; Sequence 1, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310US
; CURRENT APPLICATION NUMBER: US/09/128,354
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-128-354-1

Alignment Scores:
Pred. No.:      6,31e-264      Length:      4015
Score:          4996.00      Matches:      945
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      99.56%      Indels:      0
DB:              4          Gaps:      0

US-08-951-733-14 (1-949) x US-09-128-354-1 (1-4015)

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DB      422 CTGCCCAACACAGCTGACCGACGCACTGGCGGGGAGCGGGGCGTGGGGCTGCTGCTGGCG 481

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DB      602 CAGCGCGCGCCCGCCACACGCTAGTGACCCCGAAGCGTCTGGGATGCGAAGCGGCG 661

QY      225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
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DB      662 TGGAAACCATAGCGTCAGGAGCGCGGGTTCCTCCCTGGGCGCTGCCAGCCCGGGTGGGAGG 721

QY      245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgGlyAla 264
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DB      722 AGCGCGGGGGGAGTGCACCGCAAGTCTGCGTGGCCCAAGAGGCCCGCAGGCGTGGCGCT 781

QY      265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
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DB      782 GCGCCGTGAGCGGAGCGGACGCGCCCTTGGGCGAGGGGTCTCTGGGCCCGCCACCCCGGCGAGG 841
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QY      285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluGluAla 304
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DB      842 CGTGGACCGAGTGACCGTGTCTGTGTGGGTTCACCTGCCAGACCCCGCAAGAAGCC 901

QY      305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324
      |||
DB      902 ACCTCTTTGGAGGTGGCTCTCTGGCAGCGGCCACTCCACCACCTCCGTGGGCCGCCAG 961

QY      325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344
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DB      962 CACCACGCGGGGCCCGCCATCCATCGCGGCCACCACTGCTCCCTGGGACACGCGCTTCC 1021

QY      345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364
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DB      1022 CCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGGGACCAAGGAGCAGCTGCGG 1081

QY      365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384
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DB      1082 CCCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTCGTGGAG 1141

QY      385 ThrLeuPheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu 404
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DB      1142 ACCATCTTCTGGTTCAGGCCCTGGATGCCAGGACTCCCGCAGGTGGCCCGCCTG 1201

QY      405 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln 424
      |||
DB      1202 CCCCAGCGCTACTGGCAATGCGGCCCTGTTTGTGAGCTGCTTGGGAACACACGCGCAG 1261

QY      425 CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla 444
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DB      1262 TGCCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTCGAGCTCGGTGACCCCGCAGCA 1321

QY      445 AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp 464
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DB      1322 GCGGTGTCTGTGCCGCGAGAAGCCCGAGGCTCTGTGCGGCCCGCCCGAGGAGGAGAC 1381

QY      465 ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr 484
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QY      485 GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis 504
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DB      1442 GCGTTCGTGGGCGCTGCTGCGCGGTGGTGGTCCCGCAGGCTCTGCGGCTCCAGGCAC 1501

QY      505 AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys 524
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DB      1502 AACGAACGCGCTTCTCTCAGGAACCAAGAAGTTCTATCTCCTGTGGGAAGCATGCGCAAG 1561

QY      525 LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg 544
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QY      545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluLeuLeuAla 564
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      |||
DB      1682 AAGTTCTCTGCACTGGCTGATGAGTGTACGTGCTGCTGAGCTGCTCAGGTCTTCTTTTAT 1741

QY      585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604
      |||
DB      1742 GTCAGGAGACCACTGTTTCAAGAAGACAGGCTCTTTTCTACCGGAGAGTGTCTGAGAC 1801

QY      605 LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
      |||
DB      1802 AGTTGCAAGGATTTGGAATCAGACGACTTGAAGAGGGTGCAGCTGGGGAGCTGTGCG 1861

QY      625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
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DB      1862 GAAGCAGAGGTTCAGGCAGCATCGGAAGCAGCGCCGCTGCTGACGTCCAGACTCCGC 1921

QY      645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664
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Db 1982 AGAACGTTCCGACAGAAAGAGGGCGGACGCTCTCACCTCGAGGGTGAAGGACACTGTT 2041
QY SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704
Db 2042 AGCGTGCTCAACTACGAGGGGCGGCGGCCGCTCTCTGGCGCTCTGTGCTGGGC 2101
QY LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
Db 2102 CTGGAGATATCCACAGGCGCTGCGCACCTTCTGCTGCTGCTGCGGGCCAGACCCG 2161
QY ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
Db 2162 CCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGCTACGACCATCCCCAG 2221
QY AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764
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Db 2282 CGGTATGCGGTGTCCAGAAAGGCCGCCATGGGCACGTCCGCAAGGCTTCAAGAGCCAC 2341
QY ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804
Db 2342 GTCTCTACCTTGACAGACCTCAGCGGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG 2401
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Db 2402 ACCAGCCGCTGAGGAGTCCGTCGTCTATCGACAGAGTCTCTCCCTGAATGAGGCCAGC 2461
QY SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844
Db 2462 AGTGGGCTCTTCGACGCTCTTCCTACGCTTCATGTGCCACACCGCTGCGCATCAGGGGC 2521
QY LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
Db 2522 AAGTCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTC 2581
QY SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgAspGlyLeu 884
Db 2582 AGCCTGTGTACGGCGACATGGAGAAAGCTGTTTGGGGGATTGCGGGGACGGGCTG 2641
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Db 2642 CTCTCGGTTTGGTGGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAACC 2701
QY PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
Db 2702 TTCTCAGGACCTGTCGAGGTGTCCTGTAGTATGGCTGGCTGGTGAACCTGCGGAG 2761
QY ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
Db 2762 ACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTGTTTCAGATG 2821
QY ProAlaHisGlyLeu 949
Db 2822 CCGGCCACGGCCTA 2836
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RESULT 7

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US-09-675-321-1
; Sequence 1, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
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; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-09-675-321-1

Alignment Scores:
Pred. No.: 6,31e-264 Length: 4015
Score: 4996.00 Matches: 945
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.56% Indels: 0
DB: 4 Gaps: 0

US-08-951-733-14 (1-949) x US-09-675-321-1 (1-4015)

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QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGGCGTCCCGCTGCGAGCGCGTCCCTCCTGCTGCGACGCCACTACCCGCGAGGTGCTG 121
QY 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCCTGCGCCACGTTGTCGCGCGCTGGGGCCCGCAGGGCTGGCGCTGGTGCAGCGGG 181
QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCCGCGGCTTTCGCGCGCTGGTGGCCAGTGGCTGTGTCGCTGGGAGCGCA 241
QY 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGCGCGCCCGCCCGCCCGCTCTCTCCGCGAGGTGCTGCTGAAGAGGTGGTGCC 301
QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTGTCAGAGGTGTGCGAGCGCGCGCGAAGAACGTCGTGGCTTCGGCTTCGCG 361
QY 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGACGGGGCGCGCGGGGCCCCCGAGGCTTTCACCCAGCGTGCAGGTG 421
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
Db 422 CTCGCCCAACACGCTGACCGACGCTGCGGGGAGCGGGCGCTGGGGGCTGCTGCTGCG 481
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Db 482 CGCGTGGGCGACGACGTGCTGGTTCACCTGCTGCGACGCTGCGGCTCTTGTGCTGCTG 541
QY 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGCGCTTACCGAGGTGTCGGGCGCGCGCTGTACCGAGTTCGGCGTCCACT 601
QY 205 GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
Db 602 CAGCGCGCGCGCGCGCGCGCGCTAGTGGACCCCGAAGGCGTCTGGGATCGGACGGGCC 661
QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
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662 TGGAAACCATACGCTCAGGAGCGCGGGTCCCGCTGGGCTGCCAGCCCGGGTGGCAGG 721 Db
245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264 Qy
722 AGGCGCGGGGACGTGCGCAGCCGAAGTCTGCCGTGGCCAAAGAGGCCAGCGCTGGCGCT 781 Db
265 AlaProGluProGluArgThrProValGlyGlnGlySerThrAlaHisProGlyArgThr 284 Qy
782 GCCCCTGAGCGGAGCGACGCCGCTGGGAGGGGCTCTGGGCCCCACCCGGGAGGAGC 841 Db
285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304 Qy
842 CGTGGACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCACACCCGCCGAAGAGCC 901 Db
305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324 Qy
902 ACCCTCTTTGGAGGTGGCGCTCTCGCACCGCGCCACTCCCAACCCATCCGTGGCGCCAG 961 Db
325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344 Qy
962 CACCACGGGCGCCCCCATCCATCGCGGCCACACGCTCCCTGGGACAGCCCTGTGCC 1021 Db
345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364 Qy
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545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla 564 Qy
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585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604 Qy
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625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644 Qy
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645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664 Qy
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745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764 Qy
2222 GACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGGT 2281 Db
765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784 Qy
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2342 GTCTCTACCTTGACAGACCTCCAGCCGTATACGTGACAGATTGCTGGGTCTACCTCAGAG 2401 Db
805 ThrSerProLeuArgAspAlaValIleLeuGlnSerSerSerLeuAsnGluAlaSer 824 Qy
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925 ThrValValAsnPheProValGluAspLalaLeuGlyGlyThrAlaPheValGlnMet 944 Qy
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945 ProAlaHisGlyLeu 949 Qy
2822 CCGGCCCCACGGCCCTA 2836 Db

RESULT 8
US-09-052-919-1
Sequence 1, Application US/09052919
Patent No. 644650
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-00360005
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (htrr)"
US-09-052-919-1
Alignment Scores:
Pred. No.: 6,31e-264 Length: 4015
Score: 4996.00 Matches: 945
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.56% Indels: 0
DB: 4 Gaps: 0
US-08-951-733-14 (1-949) x US-09-052-919-1 (1-4015)
QY 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
DB 2 CAGCGCTGGCTCTGCTGGCACGTGGGAGAGCCCTGGCCCGCCACCCCGCATGCCG 61
QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
DB 62 CGCGCTCCCGCTGCCGAGCCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCTG 121
QY 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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DB 242 CGCGCGCCCGCGCGCCCTCTTCGCCAGGTGCTCTGCTGAAGGAGCTGTGGGCC 301
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DB 362 CTGCTGGACGGGGCGCGGGGGCGCCCGCCAGAGGCTTCACCCAGCGGTGGCGAGCTAC 421
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
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DB 602 CAGCGCGCGCGCGCGCGCGCTAGTGGACCCCGAAGCGCTCTGGGATGCCAGCGGCC 661
QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
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| QY | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
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| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| DB | 842 | CCTGACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACCCGCCGAAGAGCC | 901 |
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| DB | 902 | ACCTCTTGGAGGTGGCTCTCTGCGACCGCCCACTCCACCAATCCGTGGCGGCCAG | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| DB | 962 | CACCACGCGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACAGCGCTGTCCC | 1021 |
| QY | 345 | ProValTrpAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluLeuArg | 364 |
| DB | 1022 | CCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGCGGCACAAAGAGCAGTGGG | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| DB | 1082 | CCCTCTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTCTGGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| DB | 1142 | ACCATCTTCTGGTTCAGGCGCTGGATGCCAGGACTCCCGCAGGTGGCCGCGCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
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| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| DB | 1262 | TGCCCCCTACGGGTGCTCTCAAGACGCACCTGCCCGCTGCGAGCTGCGGTCACCCCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| DB | 1322 | GCCGGTGTCTGTGCCGAGAGGCCAGGCGCTGTGGCGGCCGCCAGGAGGAGC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| DB | 1382 | ACAGACCCCGTCGCTGGTGCAGCTGTCCGCCACACAGCAGCCCTTGGCAGGTGTAC | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| DB | 1442 | GGCTTCGTGGGGCCCTGCTGGCGCGGCTGTGTGCCCGCCAGGCGCTCTGGGGCTCC | 1501 |
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| QY | 565 | LysPheLeuHisTrpLeuMetSerValTrpValValGluLeuLeuArgSerPheTyr | 584 |
| DB | 1682 | AAGTTCCTGCACCTGCTGATGAGTGTACGTCTGCTGAGCTGCTCAGGTCTTCTTTAT | 1741 |
| QY | 585 | ValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| DB | 1742 | GTACCGGAGACCACTTTCAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAG | 1801 |

RESULT 9

| | | | |
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| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 |
| DB | 1802 | AGTTTGCAAGCATTTGAATCAGACACACTTGAAGAGGGTCAGCTCGGGAGCTGTGG | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| DB | 1862 | GAAGCAGAGTTCAGCAGCATCGGAAGCCAGGCGCGCCCTGCTGACGTCCAGACTCCG | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| DB | 1922 | TTTCATCCCCAACCCCTGACGGCTGCGCGCATTTGTGAACATGGACTACCTCTGGAG | 1981 |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| DB | 1982 | AGAACGTTCCGAGAGAAAAGAGGCCGAGCGTCTACCTCGAGGTGAAGCACTGTTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
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| DB | 2102 | CTGGACGATATCCACAGGCGCTGGCGCACTTCGTGCTGCTGCGGCCAGGACCG | 2161 |
| QY | 725 | ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln | 744 |
| DB | 2162 | CGCGCTGAGCTACTTTGTCAAGGTGGATGTGAGGGGCGCTAGCACACCATCCCCAG | 2221 |
| QY | 745 | AspArgLeuThrGluValIleAlaSerIleLeuLysProGlnAsnThrTyrCysValArg | 764 |
| DB | 2222 | GACAGGCTCACGAGGTCATCGCCAGCATCATCAACCCAGAACACGTACTGCGTGGT | 2281 |
| QY | 765 | ArgTyrAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
| DB | 2282 | CGGTATGCGTGTCCAGAAGCGGCCCATGGCAGCTCCGCAAGGCCCTCAAGAGCCAC | 2341 |
| QY | 785 | ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu | 804 |
| DB | 2342 | GTCTCTACCTTACAGACCTCCAGCGTACATGCGACAGTTCTGTGGCTCACCCTGCA | 2401 |
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| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly | 844 |
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| DB | 2522 | AGTCTCTAGTCCAGTCCCGAGGGATCCCGCAGGGCTCCATCTCTCCACGTGCTCTGC | 2581 |
| QY | 865 | SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu | 884 |
| DB | 2582 | AGCCTGTGCTACGCGACATGGAGAACAAGCTGTTTGGGGGATTTCGGCGGAGCGGCTG | 2641 |
| QY | 885 | LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr | 904 |
| DB | 2642 | CTCCTCGCGTTTGGTGGATGATTTCTTGTGTGGTACACCTCACCTCACCCACGCAAA | 2701 |
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; Sequence 1, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTert"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hTert) catalytic protein
; OTHER INFORMATION: component"
; US-08-912-951-1

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QY 345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364
DB 1022 CGGGTGACCGCGAGACCAACGACTTCTCTACTCTCAGCGGACCAAGAGCAGTGGCG 1081
QY 365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgLeuValGlu 384
DB 1082 CCCCTCTTCTACTCAGCTCTCTAGGCGCCAGCTGACTGGCGCTCGGAGGCTCTGGAG 1141
QY 385 ThrilePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu 404
DB 1142 ACCATCTTCTGGGTTCAGGCGCTGGATGCGAGGACTCCCGCAGGTTCGCCCGCTG 1201
QY 405 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln 424
DB 1202 CCCCAGCGCTACTGGCAATCGGCGCCCTGTTTCTGGAGCTGCTTGGGACCAACCGCGAG 1261
QY 425 CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla 444
DB 1262 TGCCCTCAGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCAACCCAGCA 1321
QY 445 AlaGlyValCysAlaArgLysProGlnGlySerValAlaAlaProGluGluAsp 464
DB 1322 GCCGTGTCTGTGCCGGGAAGCCCCAGGCTCTGTGGCGGCCCCCGAGGAGGAGAC 1381
QY 465 ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr 484
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QY 485 GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis 504
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QY 505 AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys 524
DB 1502 AACGAACCCCGCTTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAAG 1561
QY 525 LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg 544
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QY 585 ValThrGluThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerValTrpSer 604
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DB 1862 GAAGCAGAGGTTCAGSCACATCGGAAGCCAGGCGCCCTGCTGACGTCCAGACTCCGC 1921
QY 645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664
DB 1922 TTATCCCCAAGCTGACGCGCTGCGCGCGATTTGGAACATGAGACTAGCTGTGGAGCC 1981
QY 665 ArgThrPheArgGluGlyArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
DB 1982 AGAACGTTCCCGCAGAGAAAAGAGGCGCGAGCTCTCACCTCGAGGGTGAAGGCAGTGTTC 2041
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QY 695 SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704
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QY 765 ArgTyrAlaValIleGlnLysAlaHisGlyHisValArgLysAlaPheLysSerHis 784
DB 2282 CGGTATGCGGTGTCAGAGGCGCCCATGGCAGCTCCGCAAGGCTTCAAGAGCCAC 2341
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DB 2402 ACCAGCCGCTGAGGAGTGCCTGTCATCGACGAGAGTCTCTCCTGAATGAGGCCAGC 2461
QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
DB 2462 AGTGGCCCTTTCGAGCTCTTCTACGCTCATGTGCCACCGCGCTGCGCATCAGGGC 2521
QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
DB 2522 AAGTCTCAGTCCAGTCCAGGCGGATCCCGCAGGCTCCATCTCTCCACGCTGCTCTGC 2581
QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
DB 2582 AGCCTGTGCTACGGGACATGGAGAACAAAGCTGTTTGGGGGATTTCGGCGGACGGGCTG 2641
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
DB 2642 CTCCTCGCTTGTGGTGGATGATTTCTTGTGTGGTGCACCTCACCTCACCGCGGAAACC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
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RESULT 10
US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
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; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3

Alignment Scores:

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Score: 4996.00 Matches: 945
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.56% Indels: 0
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US-08-951-733-14 (1-949) x US-09-733-294A-3 (1-4015)

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QY 705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
DB 2102 CTGGAGCATATCCAGAGCGCTGGCGACCTTCGTGCTGCGTGGCGCGCGAGCCG 2161
QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
DB 2162 CGCGCTGAGCTACTTGTCAAGGTGGATGTGACGGCGGTACGACACCATCCCCAG 2221
QY 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764
DB 2222 GACAGCGCTACGAGGAGTTCATCCAGCATCATCAACCCCAAGAACCTACTGCTGGCT 2281
QY 765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
DB 2282 CGGTATGCGGTGCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2341
QY 785 ValSerThrLeuThrAspGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804
DB 2342 GTCTCTACTTACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGCGAG 2401
QY 805 ThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGluAlaSer 824
DB 2402 ACCAGCGCGCTGAGGATGCGCGTCTCATCGAGCAGAGTCTCCTCAATGAGGCCAGC 2461
QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844
DB 2462 AGTGGCGCTTCGAGCTCTCTCAGCTTCATGTCCACCGCGCGCGCATCAGGCGC 2521
QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
DB 2522 AAGTCTAGCTCAGTCCAGGAGTCCCGAGGCTCCATCTCTCCACGCTGCTCTGC 2581
QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
DB 2582 AGCCTGTGCTACGCGGACATGAGAACAAAGCTGTTTGGCGGGATTCCGCGGACGGCTG 2641
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
DB 2642 CTCCTGCGTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACCGAAACCC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
DB 2702 TTCCTCAGGACCTGCTCGAGGTGCTCCTGAGTATGCTGCTGGTGGTGAACCTGCGAAG 2761
QY 925 ThrValValAsnPhenProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
DB 2762 ACAGTGGTGAATTCCTCTGTAGAAGACGAGCGCGCTGGTGGCAGCGCTTTTGTTCAGATG 2821
QY 945 ProAlaHisGlyLeu 949
DB 2822 CGGGCCACGGGCTA 2836

RESULT 11

US-08-974-549A-343
; Sequence 343, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
US-08-974-549A-343

Alignment Scores: 1.35e-263 Length: 4037
Pred. No.:

| | | | |
|--|---------|--|-----|
| Score: | 4990.00 | Matches: | 944 |
| Percent Similarity: | 99.89% | Conservative: | 0 |
| Best Local Similarity: | 99.89% | Mismatches: | 1 |
| Query Match: | 99.44% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |
| US-08-951-733-14 (1-949) x US-08-974-549A-343 (1-4037) | | | |
| QY | 5 | GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro | 24 |
| DB | 2 | CAGCGCTGCGTCTCTGCGCAGCTGGAGCCCTGGCCCCGCCACCCCGCGATGCCG | 61 |
| QY | 25 | ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu | 44 |
| DB | 62 | CGCGCTCCCGCTGCGAGCGTGCCTCTCTGCGCAGCCACTACCGGAGGTGCTG | 121 |
| QY | 45 | ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly | 64 |
| DB | 122 | CCGCTGCCACGTCTGTCGGCCCTTGGGGCCCGAGGGCTGGCGCTGGTGCAGCGCGG | 181 |
| QY | 65 | AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla | 84 |
| DB | 182 | GACCCGCGGCTTTCGCGCGCTGGTGCCAGTGCCTGGTGGCTGGCGGCGCA | 241 |
| QY | 85 | ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla | 104 |
| DB | 242 | CGCCCGCCCCCGCCCTCTCTCCGCGCAGGTCTCTCCCTGAAAGGAGCTGGTGGCC | 301 |
| QY | 105 | ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla | 124 |
| DB | 302 | CGAGTCTGCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGTGCGCTTCGCGT | 361 |
| QY | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr | 144 |
| DB | 362 | CTGCTGAGCGGCGCGCGGGCCCCCGAGGCTTCACACAGCGTGCACGCTAC | 421 |
| QY | 145 | LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg | 164 |
| DB | 422 | CTGCCCAACACGGTGACACGACACTGCGCGGGAGCGGGCGTGCCTGCTGCGC | 481 |
| QY | 165 | ArgValGlyAspAspValLeuValHisLeuLeuAlaCysAlaLeuPheValLeuVal | 184 |
| DB | 482 | CGGCTGGCGGACACGCTGTGTACCTGCTGGCAGCTGCGCGCTCTTGTGTGGTG | 541 |
| QY | 185 | AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr | 204 |
| DB | 542 | GCTCCAGCTGCGCTTACCAGGTGTGCGGCGCCCGCTGTACACAGCTGCGCGCT | 601 |
| QY | 205 | GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla | 224 |
| DB | 602 | CAGCGCGGCGCGCGCACACGCTAGTGGACCCCGAAGCGCTCTGGGATCGCAACGGCC | 661 |
| QY | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| DB | 662 | TGAACCATAGCTCAGGAGCGCGGGTCCCTGGGCTGCGACCGCGGTGGGAGG | 721 |
| QY | 245 | ArgArgGlyCysSerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla | 264 |
| DB | 722 | AGCGCGGGGCGAGTCCAGCCAGCTGTGCCGTGCCCAAGAGCCCGCGGTGGCGT | 781 |
| QY | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| DB | 782 | GCCCTTGAGCGGAGCGGCGCGCTTGGCAGGGGTCTGGGCCCGCCACCCGGGCGAGC | 841 |
| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| DB | 842 | CGTGGACCGAGTACCGTGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 901 |
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| DB | 902 | ACCTCTTTGGAGGCTGCTCTCTGCGACGCGCCACTCCACCCATCCGTGGCGCCAG | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |

| | | | |
|----|------|--|------|
| DB | 962 | CACCACGCGGCGCGCCATCCACATCGCGCCACACGTCCTCGGACACGCTGTGCC | 1021 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| DB | 1022 | CCGCTGTACCGCGAGACCAAGCACTTCTCTACTCTCAGCGACACAGGACAGCTCGG | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgLeuValGlu | 384 |
| DB | 1082 | CCCTCTCTCTACTCTAGCTCTCTGAGGCCAGCGCTGACTGGCGCTCGGAGGCTCGTGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| DB | 1142 | ACCATCTTCTGCTGCTCCAGCGCTGATGCCAGGACCTCCCGCAGGTGTGCCCGCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
| DB | 1202 | CCCCAGCGCTACTGGCAATGCGGCCCTGTTCTTGGAGCTGCTGGGAACACGCGCAG | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| DB | 1262 | TGCCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGGGCTACCCCGCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| DB | 1322 | GCCGGTGTCTGTCGCGGAGAACGCCAGGCTCTGTGGCGGCCCGCAGGAGGAGAC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| DB | 1382 | ACAGACCCCGCTGCGCTGGTGCAGCTCTCCGCCACACAGCAGCCCTGGCAGGTGTAC | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| DB | 1442 | GGCTTGTGGGCGCTGCTGCGCGGCTGGTGGCCCCCAGCGCTCTGGGCTCCAGGCAC | 1501 |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 |
| DB | 1502 | AACGAACCGCGCTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAAG | 1561 |
| QY | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 |
| DB | 1562 | CTCTCGCTGAGGAGCTGAGTGGAAAGATGAGCGTGGGAGCTGCGCTGGCGCAGG | 1621 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla | 564 |
| DB | 1622 | AGCCAGGGGTGCTGTTCGCGCGCAGACGCTGCTGCTGAGGAGATCTCTGGCC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr | 584 |
| DB | 1682 | AAGTCTCTGCACTGGGTGATGAGTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1741 |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| DB | 1742 | GTACGAGAGACACAGCTTCAAAAGAACAGCTCTTTTCTACCGCGGAGGTGCTGGAGC | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 |
| DB | 1802 | AAGTTCGAAGCAATGGAATCAGACACCACTTGAAGAGGTGAGCTGCGGGAGCTGTCG | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| DB | 1862 | GAAGCAGAGGTACGGCAGCATCGGAAGCCAGCGCCCTGCTGAGTCCAGACTCCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| DB | 1922 | TTCATCCCCAAGCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCTGTGGAGCC | 1981 |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| DB | 1982 | AGACGCTTCGCGAGAGAAAGGCGCGCTACCTCGAGGGTGAAGGACCTGCTTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |

Db 2042 AGCGTGCTCAACTACGAGCGGCGCGCCGCCCTCTGGGGCCCTCTGTGCTGGGC 2101
QY 705 Leuaspaspiliehialatrpargthrphelvalleuargvalargalaalasparg 724
Db 2102 CTGGACGATATCCACAGCGCGCTGGCGCACCTTCGTGCTGGCGGCCAGACCGC 2161
QY 725 ProProGluLeuTyPheValLysValAspValThrGlyAlaTyAspThrIleProGln 744
Db 2162 CGCGCTGAGCTGACTTTGTCAAGGTGGATGTGACGGCGGGGTAGCACACCATCCCCCAG 2221
QY 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyCysValArg 764
Db 2222 GACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGGT 2281
QY 765 ArgTyAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
Db 2282 CGGTATGCGGTGTCAGAAAGCCGCCCATGGGACGTCCGCAAGGCCCTTCAAGAGCCAC 2341
QY 785 ValSerThrLeuThrAspLeuGlnProTyMetArgGlnPheValAlaHisLeuGlnGlu 804
Db 2342 GTCTCTACTTGACAGACTCCAGCGGTACATGCGACAGTTCGTGGCTCACCCTGAGGAG 2401
QY 805 ThrSerProLeuArgAspAlaValValIleGlnSerSerSerLeuAsnGluAlaSer 824
Db 2402 ACCAGCGCGCTGAGGATGCGGTCTGTCATCGACGAGAGCTCTCCCTGAATGAGGCCAGC 2461
QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844
Db 2462 AGTGCGCTTCGAGCGTCTCTACGCTTCATGTGCCACCGCGCTCGCATCAGGGGC 2521
QY 845 LysSerTyValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
Db 2522 AAGTCTACGTCCAGTCCAGGGGATCCCGAGGCTCCATCTCTCCACGCTGCTCGC 2581
QY 865 SerLeuCysTyArgLysMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
Db 2582 AGCCTGTCTCAGCGGACATGAGAAACAAGCTGTTTGGCGGATTCGCGGCGACGGCTG 2641
QY 885 LeuLeuArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
Db 2642 CTCCTGCGCTTGGTGATGATTTCTGTGTGTGACACCTCACCTCACCCAGCGAAACC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyGlyCysValValAsnLeuArgLys 924
Db 2702 TTCCTCAGACCTGCTCGAGGTCTCCCTGAGTATGCTGGGTGGTGAACCTTGGGAG 2761
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
Db 2762 ACAGTGTGAACCTCCCTGTAGAACGACGCGCCCTGGGTGGCAGCGCTTTTGTTCAGATG 2821
QY 945 ProAlaHisGlyLeu 949
Db 2822 CGGCGCCACGGCCTA 2836

RESULT 12
US-08-974-549A-638
; Sequence 638, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 638:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note= "hTERT-encoding sequence employing
OTHER INFORMATION: alternative codon distributions for
OTHER INFORMATION: E. coli (all genes)"
US-08-974-549A-638

Alignment Scores:
Pred. No.: 8,97e-259 Length: 3396
Score: 4900.00 Matches: 927
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.65% Indels: 0
DB: 3 Gaps: 0

US-08-951-733-14 (1-949) x US-08-974-549A-638 (1-3396)

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QY 883 GlyLeuLeuAArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAla 902
Db 2581 GGTGTTGTTGAGATGGTTGATGATTTTGTGTTACTCCACATTTGACTCATGCT 2640
QY 903 LysThrPheLeuAArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 922
Db 2641 AAACTTTTTCAGAACCTTTGTTAGAGGTGTTCCAGAAATATGGTTGTTGTTAAATTTG 2700
QY 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942
Db 2701 AGAAAACTGTTGTTAAATTTCCAGCTTGAAGATGAAGCTTTTGGTGGTACTGCTTTGTT 2760
QY 943 GlnMetProAlaHisGlyLeu 949
Db 2761 CAAATGCCAGCTCATGTTTG 2781

RESULT 15

US-08-974-549A-641
; Sequence 641, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 641:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..3396
; OTHER INFORMATION: /note= "hTERT-encoding sequence employing
; OTHER INFORMATION: alternative codon distributions for
; OTHER INFORMATION: yeast (high expressing genes)"
US-08-974-549A-641

Alignment Scores:

Pred. No.: 8 97e-259 Length: 3396
Score: 4900.00 Matches: 927
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.65% Indels: 0
DB: 3 Gaps: 0

US-08-951-733-14 (1-949) x US-08-974-549A-641 (1-3396)

QY 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42
Db 1 ATGCCAAGAGCTCCCAAGATGTAGAGCTTTTAGATCTTTTGTGAGATCTCTACACAGAGAA 60
QY 43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGln 62
Db 61 GTTTTGCCATTTGGCTACTTTCTGTTAGAGATTGGGTCACAGAGTTGGAGATTGGTTCAA 120
QY 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 82
Db 121 AGAGGTGACCCAGCTGCTTTCAGAGCTTTTGGTTGCTCAATGTTGGTTTGTGTTCCATGG 180
QY 83 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
Db 181 GACGCTAGACCCACCACAGCTGCTCCATCTTTTCAGACAGAGTTTCTTTGTTGAAGGAATG 240
QY 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 122
Db 241 GTTGCTAGAGTTTTCGAAGATTGTGTGAAGAGGTGTGAAGAGGTGTGAAGAGCTTTTGGCT 300
QY 123 PheAlaLeuLeuAspGlyAlaAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 142
Db 301 TTCGCTTTGTTGGACGGTGTAGAGGTGCTCCACAGAGAGCTTTCTACTACTTCTGTAGA 360
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Job time : 189.779 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2003, 08:32:46 ; Search time 49.3061 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 4 | 901 | 100.0 | 4015 | 4 | US-09-430-323-224 |
| 5 | 901 | 100.0 | 4015 | 4 | US-09-572-423B-3 |
| 6 | 901 | 100.0 | 4015 | 4 | US-09-128-354-1 |
| 7 | 901 | 100.0 | 4015 | 4 | US-09-675-321-1 |
| 8 | 901 | 100.0 | 4015 | 4 | US-09-052-919-1 |
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| 37 | 159 | 17.6 | 389 | 4 | US-09-430-323-62 | Sequence 8, Appl1 |
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ALIGNMENTS

RESULT 1
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; Sequence 224, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
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; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:

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; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; MOLECULE TYPE: cDNA
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Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGTCGTCGGAGCCAGAACGTTCCGACAGAAAAGAGGCGGAGGCTCTCACTCGAGGGT 120
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| : | REGISTRATION NUMBER: | 36,429 |
| : | REFERENCE/DOCKET NUMBER: | 015389-002610US |
| : | TELECOMMUNICATION INFORMATION: | |
| : | TELEPHONE: | (415) 576-0200 |
| : | TELEFAX: | (415) 576-0300 |
| : | INFORMATION FOR SEQ ID NO: 1: | |
| : | SEQUENCE CHARACTERISTICS: | |
| : | LENGTH: | 4015 base pairs |
| : | TYPE: | nucleic acid |
| : | STRANDEDNESS: | single |
| : | TOPOLOGY: | linear |
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TYPE: nucleic acid
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transcriptase (hrrt) catalytic protein
component"
US-08-854-050-224

Query Match 100.0%; Score 901; DB 3; Length 4015;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CGTGTGGAGCCAGAACAGTTCCGACAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGT 120
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Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
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Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTA 60
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RESULT 5
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; Sequence 3, Application US/09572423B

Patent No. 6331399
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: William A. Gaarde
APPLICANT: Edward Wanciewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0462
CURRENT APPLICATION NUMBER: US/09/572.423B
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 3
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)...(3454)
US-09-572-423B-3

Query Match 100.0%; Score 901; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTA 60
DB 1909 GTCCAGACTCCGCTTCCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTA 1968
QY 61 CGTCGTGGAGCCAGAACGTTCCGAGAGAAAGAGGGCGGCGTCTCACCTCGAGGGT 120
DB 1969 CGTCGTGGAGCCAGAACGTTCCGAGAGAAAGAGGGCGGCGTCTCACCTCGAGGGT 2028
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DB 2029 GAAGGCACATGTTCCAGCTGCTCAACTACGAGCGGGCGGCGCCCGGCTCTTGGGCGC 2088
QY 181 CTCTGTGCTGGGCTTGAGGATATCCACAGGGCTGCGGCACCTTCTGCTGCTGTGGC 240
DB 2089 CTCTGTGCTGGGCTTGAGGATATCCACAGGGCTGCGGCACCTTCTGCTGCTGTGGC 2148
QY 241 GGGCCAGGACCGCCCGCTGAGTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 300
DB 2149 GGGCCAGGACCGCCCGCTGAGTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 2208
QY 301 CACCATCCCGCAGGACAGGCTCAGGAGGTCTACGCGGATCATCAAAACCCAGAACAC 360
DB 2209 CACCATCCCGCAGGACAGGCTCAGGAGGTCTACGCGGATCATCAAAACCCAGAACAC 2268
QY 361 GTACTGCTGCTGGTATGCCGTGTCAGAGGGCGGCCATGGGCGAGTCCGCAAGGC 420
DB 2269 GTACTGCTGCTGGTATGCCGTGTCAGAGGGCGGCCATGGGCGAGTCCGCAAGGC 2328
QY 421 CTTCAAGAGCCAGCTCTACCTTGACAGACCTCCAGCGGTACATCGGACAGTTCGTGGC 480
DB 2329 CTTCAAGAGCCAGCTCTACCTTGACAGACCTCCAGCGGTACATCGGACAGTTCGTGGC 2388
QY 481 TCACCTGACGAGACAGGCGGCTGAGGATGCGTCTGTCATCGAGCAGCTCCCTCCCT 540
DB 2389 TCACCTGACGAGACAGGCGGCTGAGGATGCGTCTGTCATCGAGCAGCTCCCTCCCT 2448
QY 541 GAATGAGGCGCAGTGGCTCTTCCAGCTGCTTGTCAAGGTGGATGTGACGGGCGCGCT 600
DB 2449 GAATGAGGCGCAGTGGCTCTTCCAGCTGCTTGTCAAGGTGGATGTGACGGGCGCGCT 2508
QY 601 GGGCATCAGGGGAACTCTCAGACCTGTCAGGGGATCCCGAGGGTCCATCTCTC 660
DB 2509 GGGCATCAGGGGAACTCTCAGACCTGTCAGGGGATCCCGAGGGTCCATCTCTC 2568
QY 661 CACGCTGCTGTCAGGCTGTCGAGCGACATGGAGAACAGCTGTTTGGCGGGATTCG 720
DB 2569 CACGCTGCTGTCAGGCTGTCGAGCGACATGGAGAACAGCTGTTTGGCGGGATTCG 2628
QY 721 GGGGACGGGCTGCTCTCGCTTGGTGGATGATTTCTTGGTGACACCTCACCTCTAC 780
DB 2629 GGGGACGGGCTGCTCTCGCTTGGTGGATGATTTCTTGGTGACACCTCACCTCTAC 2688
QY 781 CCACGGGAAAACCTTCTCAGACCTGTCGAGGTGTCCTGAGTGTGCGGTGGT 840
DB 2689 CCACGGGAAAACCTTCTCAGACCTGTCGAGGTGTCCTGAGTGTGCGGTGGT 2748
QY 841 GAACTTGGGAGACAGTGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGCAGGC 900
DB 2749 GAACTTGGGAGACAGTGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGCAGGC 2808
QY 901 T 901
DB 2809 T 2809

Db 2629 GCGGACCGGGTCTCTCGCTTGGTGATGAATTCCTGTGTGGTACACCTCACTCAC 2688
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QY 901 T 901
Db 2809 T 2809

RESULT 6
US-09-128-354-1
; Sequence 1, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE OF INVENTION: 015389-003310US
; CURRENT APPLICATION NUMBER: US/09/128,354
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cdna
US-09-128-354-1

Query Match 100.0%; Score 901; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCAGACTCGGCTTCATCCCAAGCCTGACGGGCTCGGGCCGATTTGTGAACATGGACTA 60
Db 1909 GTCCAGACTCGGCTTCATCCCAAGCCTGACGGGCTCGGGCCGATTTGTGAACATGGACTA 1968
QY 61 CGTCGTGGGAGCCAGAACGTTCCGCGAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGT 120
Db 1969 CGTCGTGGGAGCCAGAACGTTCCGCGAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGT 2028
QY 121 GAAGGCACTGTCAGCGTGTCTCACTACGAGCGGGCGGGCGGCTCTCTGGGCGC 180
Db 2029 GAAGGCACTGTCAGCGTGTCTCACTACGAGCGGGCGGGCGGCTCTCTGGGCGC 2088

QY 181 CTCCTGTGGCTGGACGATATCCACAGGSCCTGGGCGACCTTCCTGCTCGGTGTGGC 240
Db 2089 CTCCTGTGGCTGGACGATATCCACAGGSCCTGGGCGACCTTCCTGCTCGGTGTGGC 2148
QY 241 GCGCCAGAGCCCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 300
Db 2149 GCGCCAGAGCCCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 2208
QY 301 CACCATCCCCCAGGACAGGCTCACGGAGGTCTATCCCGAGCATCATCAAAACCCCAACAC 360
Db 2209 CACCATCCCCCAGGACAGGCTCACGGAGGTCTATCCCGAGCATCATCAAAACCCCAACAC 2268
QY 361 GTACTGCTGGTGTGCTGATGCGGTGCTCAGAAAGCCGCCCATGGGCGAGTCCGCAAGGC 420
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QY 421 CTTCAAGAGCCACGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGGC 480
Db 2329 CTTCAAGAGCCACGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGGC 2388
QY 481 TCACCTGCAGGACAGCAGCCGCTGAGGATGCCGTCTCATCGAGCAGAGCTCTCCCT 540
Db 2389 TCACCTGCAGGACAGCAGCCGCTGAGGATGCCGTCTCATCGAGCAGAGCTCTCCCT 2448
QY 541 GAATGAGGCCACGAGTGGCTCTTTCGAGCTCTTCTACGCTTCTATGTGCGACACGCGGT 600
Db 2449 GAATGAGGCCACGAGTGGCTCTTTCGAGCTCTTCTACGCTTCTATGTGCGACACGCGGT 2508
QY 601 GCGCATCAGGGGCAAGTCTTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTC 660
Db 2509 GCGCATCAGGGGCAAGTCTTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTC 2568
QY 661 CACGCTGCTCTGCAGCCTGTGCTACGGCGACATGAGAACAGCTGTTTGGGGGATTCG 720
Db 2569 CACGCTGCTCTGCAGCCTGTGCTACGGCGACATGAGAACAGCTGTTTGGGGGATTCG 2628
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Db 2629 GCGGACGCGGTGCTCTCGCTTGTGGTGAATTCCTTGTGGTGAACACCTCACTCAC 2688
QY 781 CCACGCGAAAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT 840
Db 2689 CCACGCGAAAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT 2748
QY 841 GAACCTGCGGAAGACAGTGGTGAACCTCCCTGTGAGAACAGAGGCCCTGGGTGGCACGGC 900
Db 2749 GAACCTGCGGAAGACAGTGGTGAACCTCCCTGTGAGAACAGAGGCCCTGGGTGGCACGGC 2808
QY 901 T 901
Db 2809 T 2809

RESULT 7
US-09-675-321-1
; Sequence 1, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

;< br>LENGTH: 4015< br>TYPE: DNA< br>ORGANISM: Homo sapiens< br>FEATURE:< br>NAME/KEY: CDS< br>LOCATION: (36)..(3454)< br>OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)< br>US-09-675-321-1

Query Match 100.0%; Score 901; DB 4; Length 4015;

Best Local Similarity 100.0%; Pred. No. 3.9e-210;

Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACCCGCTTCATCCCAAGCCTGACGGCTGCGCGCGATGTGAACATGACATA 60< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 1909 GTCCAGACCCGCTTCATCCCAAGCCTGACGGCTGCGCGCGATGTGAACATGACATA 1968< br>QY 61 CGTCGTGGAGCCAGAACCTTCGCGAGAGAAAGAGGCGCGCTCACCTCGAGGGT 120< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 1969 CGTCGTGGAGCCAGAACCTTCGCGAGAGAAAGAGGCGCGCTCACCTCGAGGGT 2028< br>QY 121 GAAGGACATGTCAGGCTGCTCACTACAGGGGCGCGCGCGCTCTCTGGGCGC 180< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2029 GAAGGACATGTCAGGCTGCTCACTACAGGGGCGCGCGCGCTCTCTGGGCGC 2088< br>QY 181 CTCGTGCTGGCGTGGAGCATATCCACAGGCGCTGCGCACCTTCGTGCTGCTGGC 240< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2089 CTCGTGCTGGCGTGGAGCATATCCACAGGCGCTGCGCACCTTCGTGCTGCTGGC 2148< br>QY 241 GSCCCAGGACCCGCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGA 300< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2149 GSCCCAGGACCCGCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGA 2208< br>QY 301 CACCATCCCCAGGACAGGCTCAGGAGTCAATCGGCAGCATCATCAAAACCCAGAACAC 360< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2209 CACCATCCCCAGGACAGGCTCAGGAGTCAATCGGCAGCATCATCAAAACCCAGAACAC 2268< br>QY 361 GTACTGCTGCTGCGTATGCGTGTCCAGAGGCGCGCCATGGCAGCTCGCAAGGC 420< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2269 GTACTGCTGCTGCGTATGCGTGTCCAGAGGCGCGCCATGGCAGCTCGCAAGGC 2328< br>QY 421 CTTCAAGACCCACGCTCTTACCTTGACAGACCTCCAGCGGTACATCGGACAGTTCGTGGC 480< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2329 CTTCAAGACCCACGCTCTTACCTTGACAGACCTCCAGCGGTACATCGGACAGTTCGTGGC 2388< br>QY 481 TCACCTCAGGAGACAGCCCGCTGAGGATCGCTGTCATCGAGCAGAGTCTCTCCCT 540< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2389 TCACCTCAGGAGACAGCCCGCTGAGGATCGCTGTCATCGAGCAGAGTCTCTCCCT 2448< br>QY 541 GAATGAGGCGCAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCGCACCGCCCT 600< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2449 GAATGAGGCGCAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCGCACCGCCCT 2508< br>QY 601 GGCATCAGGGGCAAGTCTTACGTCCAGTGCAGGGGATCCGCGAGGGTCCATCTCTCTC 660< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2509 GGCATCAGGGGCAAGTCTTACGTCCAGTGCAGGGGATCCGCGAGGGTCCATCTCTCTC 2568< br>QY 661 CAGCTGCTCTCAGCCTGTGTACGGGACATGAGAACAGCTGTTTCGGGGGATTCG 720< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2569 CAGCTGCTCTCAGCCTGTGTACGGGACATGAGAACAGCTGTTTCGGGGGATTCG 2628< br>QY 721 GCGGACGGGCTGCTCTCGTGTGTTGATGATTTTGTGTTGACACCTCACCTCAC 780< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2629 GCGGACGGGCTGCTCTCGTGTGTTGATGATTTTGTGTTGACACCTCACCTCAC 2688< br>QY 781 CCACGGAACCTCTCTCAGGACCTGCTCGAGGTGTCCTTGAGTATGCTGCTGCTG 840< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2689 CCACGGAACCTCTCTCAGGACCTGCTCGAGGTGTCCTTGAGTATGCTGCTGCTG 2748< br>QY 841 GAATTCGGAAGACAGTGGTGAATTCCTCTAGAACAGAGGCCCTTGGTGGCACGCGC 900< br>DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||< br>DB 2749 GAATTCGGAAGACAGTGGTGAATTCCTCTAGAACAGAGGCCCTTGGTGGCACGCGC 2808

QY 901 T 901< br>DB 2809 T 2809

RESULT 8

US-09-052-919-1

; Sequence 1, Application US/09052919

; Patent No. 6444650

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Antisense Compositions for Detecting and

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/052,919

; FILING DATE: 31-MAR-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 23-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/974,549

; FILING DATE: 19-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/974,584

; FILING DATE: 19-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:

NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (hprt)";
US-09-052-919-1

Query Match 100.0%; Score 901; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 3.9e-210; Indels 0; Gaps 0;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCAGACTCGGCTTCATCCCAAGCTGACGGGCTGGGCCGATTTGACATGGACTA 60
Db 1909 GTCCAGACTCGGCTTCATCCCAAGCTGACGGGCTGGGCCGATTTGACATGGACTA 1968
Qy 61 CGTCGTGGGAGCAGAAAGCTTCCGACAGAAAGAGGCGGAGCGTCTACCTCGAGGGT 120
Db 1969 CGTCGTGGGAGCAGAAAGCTTCCGACAGAAAGAGGCGGAGCGTCTACCTCGAGGGT 2028
Qy 121 GAAGGCACTGTTACGCTGTCTCAACTACGAGCGGCGGCGGCCGCTCTCTGGGCGC 180
Db 2029 GAAGGCACTGTTACGCTGTCTCAACTACGAGCGGCGGCGGCCGCTCTCTGGGCGC 2088
Qy 181 CTCGTGCTGGGCTTGACAGATATCCACAGGGGCTGGCGACCTTCGTGCTGTGGG 240
Db 2089 CTCGTGCTGGGCTTGACAGATATCCACAGGGGCTGGCGACCTTCGTGCTGTGGG 2148
Qy 241 GGCCAGGACCGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGCGGTACGA 300
Db 2149 GGCCAGGACCGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGCGGTACGA 2208
Qy 301 CACATCCCCAGGACAGGCTCAGGAGGTATCCGCCAGCATCATCAAAACCCAGAACAC 360
Db 2209 CACATCCCCAGGACAGGCTCAGGAGGTATCCGCCAGCATCATCAAAACCCAGAACAC 2268
Qy 361 GTACTGGTGGTGGTATGCCGTGTGTCAGAGCGGCGCCATGGGACGTCGCCAAGGC 420
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Qy 481 TCACCTGCAGGAGACCGCGCTGAGGGATCGCGTCTCATCGAGCAGAGCTCCTCCCT 540
Db 2389 TCACCTGCAGGAGACCGCGCTGAGGGATCGCGTCTCATCGAGCAGAGCTCCTCCCT 2448
Qy 541 GAATGAGCGCAGAGTGGGCTCTTCGACGCTCTTCAGCTTCATGTGCCACACGCGGT 600
Db 2449 GAATGAGCGCAGAGTGGGCTCTTCGACGCTCTTCAGCTTCATGTGCCACACGCGGT 2508
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Db 2509 GCGCATCAGGGGGAAGTCTTACGTCCAGTTCGAGGGATCCGCGAGGGCTCCATCCCTC 2568
Qy 661 CACGCTCTCGACGCTGTGCTACGCGCATGAGAAACAGCTGTTTGGGGGATTCG 720
Db 2569 CACGCTCTCGACGCTGTGCTACGCGCATGAGAAACAGCTGTTTGGGGGATTCG 2628
Qy 721 GCGGAGCGGGCTGCTCTCGGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCAC 780

Db 2629 GCGGAGCGGGCTGCTCTCGGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCAC 2688
Qy 781 CCACGCGAAACACCTTCCCTCAGGACCCCTGCTCCGAGGTGCTCCCTGAGTATGCTGGTGGT 840
Db 2689 CCACGCGAAACACCTTCCCTCAGGACCCCTGCTCCGAGGTGCTCCCTGAGTATGCTGGTGGT 2748
Qy 841 GAACCTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGC 900
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Qy 901 T 901
Db 2809 T 2809
RESULT 9
US-08-912-951-1
; Sequence 1, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTRT"
; /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hTRT) catalytic protein
; OTHER INFORMATION: component"
US-08-912-951-1

Query Match 100.0%; Score 901; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCGCTTCATCCCAAGCCTGACGGGCTGGCGGATGTGAACATGACTA 60
Db 1909 GTCCAGACTCGCTTCATCCCAAGCCTGACGGGCTGGCGGATGTGAACATGACTA 1968
QY 61 GTCGTGGAGCCAGACAGTTCGCGAGAGAAAGAGGCCGAGCGTCTCACCTCAGGGT 120
Db 1969 GTCGTGGAGCCAGACAGTTCGCGAGAGAAAGAGGCCGAGCGTCTCACCTCAGGGT 2028
QY 121 GAAGCACTGTTACGCTGCTCACTACGAGCGGCGGGCGGCCGCTCTGGGGCGC 180
Db 2029 GAAGCACTGTTACGCTGCTCACTACGAGCGGCGGGCGGCCGCTCTGGGGCGC 2088
QY 181 CTCGTGCTGGGCTCGGACGATATCCACAGGCGCTGGCGCACCTTCGCTGCGGTGCG 240
Db 2089 CTCGTGCTGGGCTCGGACGATATCCACAGGCGCTGGCGCACCTTCGCTGCGGTGCG 2148
QY 241 GSCCAGAGCCGCGCTGAGCTGACTTTGTCAAGTGGATGTGAGGGCGGTACGA 300
Db 2149 GSCCAGAGCCGCGCTGAGCTGACTTTGTCAAGTGGATGTGAGGGCGGTACGA 2208
QY 301 CACCATCCCGAGGACAGGCTCACGAGGTATCCGACAGCATCATCAACCCAGAACAC 360
Db 2209 CACCATCCCGAGGACAGGCTCACGAGGTATCCGACAGCATCATCAACCCAGAACAC 2268
QY 361 GTACTGCTGGCTGGAGCCGCTGAGGATGCGCTCATCGAGCAGAGCTCTCCCT 540
Db 2369 GTACTGCTGGCTGGAGCCGCTGAGGATGCGCTCATCGAGCAGAGCTCTCCCT 2448
QY 541 GAATGAGCCAGCAGTGGCTCTTCGAGCTGTTCTACGCTTCATGTGCCACAGCCGT 600
Db 2449 GAATGAGCCAGCAGTGGCTCTTCGAGCTGTTCTACGCTTCATGTGCCACAGCCGT 2508
QY 601 GCGCATCAGGCGAGTCTAGTCCAGTCCAGGGGATCCGACGGGCTCCATCTCTC 660
Db 2509 GCGCATCAGGCGAGTCTAGTCCAGTCCAGGGGATCCGACGGGCTCCATCTCTC 2568
QY 661 CACGTGCTCTGACGCTGTGTACGGCGACATGAGAACAGCTGTTTGGGGGATTGCG 720
Db 2569 CACGTGCTCTGACGCTGTGTACGGCGACATGAGAACAGCTGTTTGGGGGATTGCG 2628
QY 721 GCGGACCGGGTGTCTCTCGCTTTGGTGGATGATTCTTGTGTTGACACCTTCACCTCAC 780
Db 2629 GCGGACCGGGTGTCTCTCGCTTTGGTGGATGATTCTTGTGTTGACACCTTCACCTCAC 2688

QY 781 CCACGCGAAACCTTCCTCAGGACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGGT 840
Db 2689 CCACGCGAAACCTTCCTCAGGACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGGT 2748
QY 841 GAACTTGGGAAGACAGTGGTGAATTCCTCTGTAAGAACAGAGGCCCTGGGTGGGCACGCG 900
Db 2749 GAACTTGGGAAGACAGTGGTGAATTCCTCTGTAAGAACAGAGGCCCTGGGTGGGCACGCG 2808
QY 901 T 901
Db 2809 T 2809

RESULT 10
US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3

Query Match 100.0%; Score 901; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCGCTTCATCCCAAGCCTGACGGGCTGGCGGATGTGAACATGACTA 60
Db 1909 GTCCAGACTCGCTTCATCCCAAGCCTGACGGGCTGGCGGATGTGAACATGACTA 1968
QY 61 GTCGTGGAGCCAGACAGTTCGCGAGAGAAAGAGGCCGAGCGTCTCACCTCAGGGT 120
Db 1969 GTCGTGGAGCCAGACAGTTCGCGAGAGAAAGAGGCCGAGCGTCTCACCTCAGGGT 2028
QY 121 GAAGCACTGTTACGCTGCTCACTACGAGCGGCGGGCGGCCGCTCTGGGGCGC 180
Db 2029 GAAGCACTGTTACGCTGCTCACTACGAGCGGCGGGCGGCCGCTCTGGGGCGC 2088
QY 181 CTCGTGCTGGGCTCGGACGATATCCACAGGCGCTGGCGCACCTTCGCTGCGGTGCG 240
Db 2089 CTCGTGCTGGGCTCGGACGATATCCACAGGCGCTGGCGCACCTTCGCTGCGGTGCG 2148
QY 241 GSCCAGAGCCGCGCTGAGCTGACTTTGTCAAGTGGATGTGAGGGCGGTACGA 300
Db 2149 GSCCAGAGCCGCGCTGAGCTGACTTTGTCAAGTGGATGTGAGGGCGGTACGA 2208
QY 301 CACCATCCCGAGGACAGGCTCACGAGGTATCCGACAGCATCATCAACCCAGAACAC 360
Db 2209 CACCATCCCGAGGACAGGCTCACGAGGTATCCGACAGCATCATCAACCCAGAACAC 2268
QY 361 GTACTGCTGGCTGGAGCCGCTGAGGATGCGCTCATCGAGCAGAGCTCTCCGAGGC 420
Db 2269 GTACTGCTGGCTGGAGCCGCTGAGGATGCGCTCATCGAGCAGAGCTCTCCGAGGC 2328
QY 421 CTTCAAGAGCCACGCTCTTACCTTGACAGCCTTCAGCGCTGACAGCTTCGTGGC 480
Db 2329 CTTCAAGAGCCACGCTCTTACCTTGACAGCCTTCAGCGCTGACAGCTTCGTGGC 2388

QY 481 TCACCTGCAGGAGACCCCGCTGAGGGATGCCGCTCATCGACAGAGCTCCCTCCCT 540
Db 2389 TCACCTGCAGGAGACCCCGCTGAGGGATGCCGCTCATCGACAGAGCTCCCTCCCT 2448
QY 541 GAATGAGCCAGCAGTGGCTCTTCGACGCTCTTCCTACGCTTCATGTCGACACACGCCGT 600
Db 2449 GAATGAGCCAGCAGTGGCTCTTCGACGCTCTTCCTACGCTTCATGTCGACACACGCCGT 2508
QY 601 GCCATCAGGGCAAGCTTACCTACGTCAGTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTC 660
Db 2509 GCCATCAGGGCAAGCTTACCTACGTCAGTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTC 2568
QY 661 CACGCTGCTCAGGCTGTGCTACGCGGACATGAGAACAACTGTTTGGGGGATTCG 720
Db 2569 CACGCTGCTCAGGCTGTGCTACGCGGACATGAGAACAACTGTTTGGGGGATTCG 2628
QY 721 CGCGGAGCGGCTCCTCGGTTTGGTGGAGATTTCTTGGTGACACCTCACCTCAC 780
Db 2629 CGCGGAGCGGCTCCTCGGTTTGGTGGAGATTTCTTGGTGACACCTCACCTCAC 2688
QY 781 CCACGGAACCTTCTCAGGACCTGTCGAGGTGTCGAGGTGTCCTGAGTATGCTGCTGGT 840
Db 2689 CCACGGAACCTTCTCAGGACCTGTCGAGGTGTCGAGGTGTCCTGAGTATGCTGCTGGT 2748
QY 841 GAATTCGCGAAGACAGTGGTGAACCTTCCCTGTAGAGACGAGGCGCTGGTGGCACGGC 900
Db 2749 GAATTCGCGAAGACAGTGGTGAACCTTCCCTGTAGAGACGAGGCGCTGGTGGCACGGC 2808
QY 901 T 901
Db 2809 T 2809

RESULT 11

US-08-974-549A-343
; Sequence 343, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
US-08-974-549A-343

Query Match 100.0%; Score 901; DB 3; Length 4037;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCAGACTCCGCTTTCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGGACTA 60
Db 1909 GTCCAGACTCCGCTTTCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGGACTA 1968
QY 61 CGTCGTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGCGGCGAGCGTCTCACCTCGAGGGT 120
Db 1969 CGTCGTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGCGGCGAGCGTCTCACCTCGAGGGT 2028
QY 121 GAAGGCACCTGTTTCAGCGTGTCTCAACTACGAGCGGGCGGCGGCCGCCGCTCTCGGCGC 180
Db 2029 GAAGGCACCTGTTTCAGCGTGTCTCAACTACGAGCGGGCGGCGGCCGCCGCTCTCGGCGC 2088
QY 181 CTCTGTGCTGGGCTTGACGATATCCACAGGGGCTGGCGCACCTTGTGTGCTGTGGG 240
Db 2089 CTCTGTGCTGGGCTTGACGATATCCACAGGGGCTGGCGCACCTTGTGTGCTGTGGG 2148
QY 241 GGCCAGAGACCCCGCGCTGAGCTGTACTTGTCAAGGTGATGTGACGGGCGGTACGA 300
Db 2149 GGCCAGAGACCCCGCGCTGAGCTGTACTTGTCAAGGTGATGTGACGGGCGGTACGA 2208
QY 301 CACCATCCCCCAGGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAC 360
Db 2209 CACCATCCCCCAGGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAC 2268
QY 361 GTACTGCGTGGTGGTATGCTGATGCCGTGTCAGAGAGGCGGCCCATCGGACGTCGCGAGGC 420
Db 2269 GTACTGCGTGGTGGTATGCTGATGCCGTGTCAGAGAGGCGGCCCATCGGACGTCGCGAGGC 2328

Db 2504 GCGCATCAGGGGCAAGTCTACGTCCAGTCCAGGGGATCCGAGGGCTCCATCCTCTC 2563
Qy 661 CACCTCTCTGACAGCTGTGCTACGGGACATGGAGAACAGCTGTTGGGGGATTCG 720
Db 2564 CACCTCTCTGACAGCTGTGCTACGGGACATGGAGAACAGCTGTTGGGGGATTCG 2623
Qy 721 GCGGAGCGGCTGCTCTCTGCTTTGGTGGATGATTTCTTGTGTGACACTCACCTTCAC 780
Db 2624 GCGGAGCGGCTGCTCTCTGCTTTGGTGGATGATTTCTTGTGTGACACTCACCTTCAC 2683
Qy 781 CCAGCGCAAAACCTTCTCAGGACCTTGGTCCGAGGTGCTCCGTGATGATGCTGCTGGT 840
Db 2684 CCAGCGCAAAACCTTCTCAGGACCTTGGTCCGAGGTGCTCCGTGATGATGCTGCTGGT 2743
Qy 841 GAACCTTCGGAAGACAGTGTGTAACCTTCCCTGTAGAGACAGAGGCCCTGGTGGCAGGC 900
Db 2744 GAACCTTCGGAAGACAGTGTGTAACCTTCCCTGTAGAGACAGAGGCCCTGGTGGCAGGC 2803
Qy 901 T 901
Db 2804 T 2804

RESULT 13

US-08-974-549A-292
; Sequence 292, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R. ✓
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4029
; OTHER INFORMATION: /note= "preliminary sequence for
; OTHER INFORMATION: human TRT cDNA insert of
; OTHER INFORMATION: plasmid pGRN121"
; US-08-974-549A-292

Query Match 99.7%; Score 898.4; DB 3; Length 4029;
Best Local Similarity 99.8%; Pred. No. 1.7e-209;
Matches 899; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGGGCGGATTTGTAACATGGACTA 60
Db 1904 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGGGCGGATTTGTAACATGGACTA 1963
Qy 61 CGTCGTGGAGCCAGAACAGTTCCGCAGAGAAAAGAGGGCGGAGCGTCTACCTCGAGGGT 120
Db 1964 CGTCGTGGAGCCAGAACAGTTCCGCAGAGAAAAGAGGGCGGAGCGTCTACCTCGAGGGT 2023
Qy 121 GAAGGCACCTGTTACAGCGTGTCAACTACGAGGGCGGGCGGCGCCCTCTCTGGGGCGC 180
Db 2024 GAAGGCACCTGTTACAGCGTGTCAACTACGAGGGCGGGCGGCGCCCTCTCTGGGGCGC 2083
Qy 181 CTCTGTCTGGGCTTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGGC 240
Db 2084 CTCTGTCTGGGCTTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGGC 2143
Qy 241 GGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGA 300
Db 2144 GGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGA 2203
Qy 301 CACATCCCCAGGACAGAGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGACAC 360
Db 2204 CACATCCCCAGGACAGAGCTCAGGAGGTATCGCCAGGATCATGCCAGCATCATCAAAACCCAGACAC 2263
Qy 361 GTACTGCTGCTGGTATGCCGTGTCCAGAGGGCGGCCCATGGGCACCTGCCCAAGGC 420
Db 2264 GTACTGCTGCTGGTATGCCGTGTCCAGAGGGCGGCCCATGGGCACCTGCCCAAGGC 2323
Qy 421 CTTCAAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGGC 480
Db 2324 CTTCAAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGGC 2383
Qy 481 TCACCTGCAGGACAGAGCCCGCTGAGGGATGCCGTGTCATCGAGGAGAGCTCCTCCT 540
Db 2384 TCACCTGCAGGACAGAGCCCGCTGAGGGATGCCGTGTCATCGAGGAGAGCTCCTCCT 2443

| | | |
|----|--------------------------------|---|
| / | FILING DATE: | 01-OCT-1996 |
| / | CLASSIFICATION: | 536 |
| / | ATTORNEY/AGENT INFORMATION: | |
| / | NAME: | Apple, Randolph T. |
| / | REGISTRATION NUMBER: | 36,429 |
| / | REFERENCE/DOCKET NUMBER: | 015389-002930US |
| / | TELECOMMUNICATION INFORMATION: | |
| / | TELEPHONE: | (415) 576-0200 |
| / | TELEFAX: | (415) 576-0300 |
| / | INFORMATION FOR SEQ ID NO: | 173: |
| / | SEQUENCE CHARACTERISTICS: | |
| / | LENGTH: | 4029 base pairs |
| / | TYPE: | nucleic acid |
| / | STRANDEDNESS: | single |
| / | TOPOLOGY: | linear |
| / | MOLECULE TYPE: | cdna |
| / | FEATURE: | |
| / | NAME/KEY: | |
| / | LOCATION: | 1..4029 |
| / | OTHER INFORMATION: | /note= "preliminary sequence for |
| / | OTHER INFORMATION: | human TRT cdna insert of |
| / | OTHER INFORMATION: | plasmid pORN121" |
| / | US-08-854-050-173 | |
| | Query Match | 99.7%; Score 898.4; DB 3; Length 4029; |
| | Best Local Similarity | 99.8%; Pred. No. 1.7e-209; |
| | Matches 899; Conservative | 0; Mismatches 2; Indels 0; Gaps 0; |
| QY | 1 | GTCAGACTCCGTTTCATCCCCAAGCCTGACGGCTTGCGGCCGTGCGGCCGATGTGAACATGGACTA 60 |
| Db | 1904 | GTCAGACTCCGTTTCATCCCCAAGCCTGACGGCTTGCGGCCGATGTGAACATGGACTA 1963 |
| QY | 61 | CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGGCGCGACGCTCTCACCTCGAGGGT 120 |
| Db | 1964 | CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGGCGCGACGCTCTCACCTCGAGGGT 2023 |
| QY | 121 | GAAGGCACCTGTTTCAGGCGTGCTCAACTACGAGCGGGCGCGCGCGCCCTCTCTGGCGCG 180 |
| Db | 2024 | GAAGGCACCTGTTTCAGGCGTGCTCAACTACGAGCGGGCGCGCGCGCCCTCTCTGGCGCG 2083 |
| QY | 181 | CCTCTGTGCTGGGCGCTGGAGCATATCCACAGGGCGCTGGCGACCTTCGTGCTGCGTGTGCG 240 |
| Db | 2084 | CCTCTGTGCTGGGCGCTGGAGCATATCCACAGGGCGCTGGCGACCTTCGTGCTGCGTGTGCG 2143 |
| QY | 241 | GGCCCAGGACCSCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGTACGA 300 |
| Db | 2144 | GGCCCAGGACCSCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGTACGA 2203 |
| QY | 301 | CACCATCCCCAGSACAGGCTCACGGAGGTCAATCGCCAGCATCATAAACCCCGAGAACAC 360 |
| Db | 2204 | CACCATCCCCAGSACAGGCTCACGGAGGTCAATCGCCAGCATCATAAACCCCGAGAACAC 2263 |
| QY | 361 | GTACTCGTGCCTGCGTATGCCGTGGTCCAGAAAGGCGGCCCATGGGCACGTCGCAAGGC 420 |
| Db | 2264 | GTACTCGTGCCTGCGTATGCCGTGGTCCAGAAAGGCGGCCCATGGGCACGTCGCAAGGC 2323 |
| QY | 421 | CTTCAAGAGCCAGCTCTCTACCTTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC 480 |
| Db | 2324 | CTTCAAGAGCCAGCTCTCTACCTTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC 2383 |
| QY | 481 | TCACCTGCAGGAGCACGCCCGCTGAGGGATGCCGTGTCATCGACGACAGCTCCCTCCCT 540 |
| Db | 2384 | TCACCTGCAGGANAAACAGCCCGCTGAGGGATGCCGTGTCATCGACGACAGCTCCCTCCCT 2443 |
| QY | 541 | GAATAGGCGCAGAGTGGCGCTCTTTCAGGCTTTTCCCTACGCTTTCATGTGCCACACGCCGT 600 |
| Db | 2444 | GAATAGGCGCAGAGTGGCGCTCTTTCAGGCTTTTCCCTACGCTTTCATGTGCCACACGCCGT 2503 |
| QY | 601 | GCGCATCAGGGGCAAGTCTCTACGTCAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTC 660 |
| Db | 2504 | GCGCATCAGGGGCAAGTCTCTACGTCAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTC 2563 |
| QY | 661 | CAGGCTGCTGTCAGCGCTGTGCTACGCGGACATGGAGAACAGCTGTTTTGCGGGGATTCG 720 |

Db 2564 CAGCTCTCTGACCGCTGTGCTACGCGGACATGGAGAACGCTGTTTCGGGGATTCG 2623
Qy 721 GCGGAGCGGCTGCTCTCTGCTTGTGGTGGATGATTTCTTGTGTGACACTCACCTCAC 780
Db 2624 GCGGAGCGGCTGCTCTCTGCTTGTGGTGGATGATTTCTTGTGTGACACTCACCTCAC 2683
Qy 781 CCACGCGAAACCTTCTCTCAGGACCCCTGCTCCAGAGTGTCCCTGAGTATGGCTGCGTGGT 840
Db 2684 CCACGCGAAACCTTCTCTCAGGACCCCTGCTCCAGAGTGTCCCTGAGTATGGCTGCGTGGT 2743
Qy 841 GAACCTGCGGAAACAGACAGTGTGTAACCTTCCCTGTAGAGACAGGCGCTGGTGGCAGCGC 900
Db 2744 GAACCTGCGGAAACAGACAGTGTGTAACCTTCCCTGTAGAGACAGGCGCTGGTGGCAGCGC 2803
Qy 901 T 901
Db 2804 T 2804

RESULT 15

US-09-430-323-173
; Sequence 173, Application US/09430323
; Patent No. 6309867

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

LENGTH: 4029 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 1..4029
; LOCATION: /note- "preliminary sequence for
; human TRT cDNA insert of
; plasmid pGRN121"
; SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-09-430-323-173

Query Match 99.7%; Score 898.4; DB 4; Length 4029;
Best Local Similarity 99.8%; Pred. No. 1.7e-209;
Matches 899; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCAGACTCCGCTTCATCCCAAGCCTGACGGCTGCGGGCTGGCCGATTTGACATGGACTA 60
Db 1904 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGCTGCGGGCTGGCCGATTTGACATGGACTA 1963
Qy 61 CGTCGTGGGAGCCAGAACGTTCCGCGACAGAGAGGCGGAGCGGTCTCACCTCGAGGGT 120
Db 1964 CGTCGTGGGAGCCAGAACGTTCCGCGACAGAGAGGCGGAGCGGTCTCACCTCGAGGGT 2023
Qy 121 GAAGGCACCTGTTACGCGTGTCTCAACTACGAGCGGCGCGGCGCCCTCTCTGGGCGC 180
Db 2024 GAAGGCACCTGTTACGCGTGTCTCAACTACGAGCGGCGCGGCGCCCTCTCTGGGCGC 2083
Qy 181 CTCTGTGCTGGCGCTGGACGATATCCACAGGCGCTGCGCACCTTCGCTGCTGGTGTGG 240
Db 2084 CTCTGTGCTGGCGCTGGACGATATCCACAGGCGCTGCGCACCTTCGCTGCTGGTGTGG 2143
Qy 241 GGCCAGGACCCCGCGCTGAGCTGTACTTTGCAAGTGGATGTGACGGCGCGGTACGA 300
Db 2144 GGCCAGGACCCCGCGCTGAGCTGTACTTTGCAAGTGGATGTGACGGCGCGGTACGA 2203
Qy 301 CACATCCCCCAGGACAGGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAACAC 360
Db 2204 CACATCCCCCAGGACAGGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAACAC 2263
Qy 361 GTACTGGTGGCTGGGTATGCGGTGTCAGAGGCGCCCATGGGCACCTGCGCAAGGC 420
Db 2264 GTACTGGTGGCTGGGTATGCGGTGTCAGAGGCGCCCATGGGCACCTGCGCAAGGC 2323
Qy 421 CTTCAAGAGCCACGTCTTACTTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGC 480
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 7, 2003, 09:31:52 ; Search time 635.99 Seconds
(without alignments)
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Perfect score: 6079

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Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 6057 | 99.6 | 4015 | 10 | US-09-990-080-1 | Sequence 1, Appli |
| 3 | 6057 | 99.6 | 4015 | 10 | US-09-843-676-224 | Sequence 224, App |
| 4 | 6057 | 99.6 | 4015 | 10 | US-09-953-052-1 | Sequence 1, Appli |
| 5 | 6057 | 99.6 | 4015 | 14 | US-10-053-758-224 | Sequence 224, App |
| 6 | 6057 | 99.6 | 4015 | 14 | US-10-208-243-1 | Sequence 1, Appli |
| 7 | 6057 | 99.6 | 4015 | 14 | US-10-054-295-224 | Sequence 224, App |
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| 10 | 6057 | 99.6 | 4015 | 14 | US-10-044-692-1 | Sequence 1, Appli |
| 11 | 6057 | 99.6 | 4015 | 14 | US-10-044-539-1 | Sequence 32, Appli |
| 12 | 5961 | 98.1 | 3396 | 10 | US-09-749-728B-32 | Sequence 1, Appli |
| 13 | 5952 | 97.9 | 3453 | 14 | US-10-205-629-1 | Sequence 1, Appli |
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| 18 | 5675 | 93.4 | 4029 | 10 | US-09-843-676-173 | Sequence 173, App |
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| 21 | 5675 | 93.4 | 4029 | 14 | US-10-054-295-173 | Sequence 173, App |
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| 23 | 3134 | 51.6 | 1866 | 14 | US-10-294-778-11 | Sequence 11, Appli |
| 24 | 2885 | 47.5 | 51552 | 9 | US-09-733-294A-30 | Sequence 30, Appli |
| 25 | 2878 | 47.3 | 4200 | 14 | US-10-044-692-6 | Sequence 6, Appli |
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| 27 | 2878 | 47.3 | 15418 | 9 | US-09-783-203-1 | Sequence 1, Appli |
| 28 | 2878 | 47.3 | 15418 | 10 | US-09-994-427A-1 | Sequence 1, Appli |
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| 33 | 2670.5 | 43.9 | 2176 | 14 | US-10-044-692-3 | Sequence 3, Appli |
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| 38 | 2591.5 | 42.6 | 2171 | 14 | US-10-053-758-100 | Sequence 100, App |
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| 41 | 2184 | 35.9 | 1314 | 14 | US-10-294-778-9 | Sequence 9, Appli |
| 42 | 2169.5 | 35.7 | 1311 | 14 | US-10-294-778-1 | Sequence 1, Appli |
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| 45 | 646 | 10.6 | 389 | 10 | US-09-843-676-62 | Sequence 62, Appli |

ALIGNMENTS

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; Sequence 3, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3

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 Query Match: 99.64% Indels: 0
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; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hprt"
; /note= "human telomerase reverse
; transcriptase (hprt) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
; US-09-843-676-224

Alignment Scores:
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Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 10 Gaps: 0

US-09-843-676-224 (1-1154) x US-09-843-676-224 (1-4015)

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RESULT 4
US-09-953-052-1
; Sequence 1, Application US/09953052
; Patent No. US20020173476A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,052
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/052,919
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-00360005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

605 LysLeuGlnSerIleGlyLeuArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
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RESULT 5

US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843

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1 FILING DATE: 06-MAY-1997
2 APPLICATION NUMBER: US 08/846,017
3 FILING DATE: 25-APR-1997
4 APPLICATION NUMBER: US 08/844,419
5 FILING DATE: 18-APR-1997
6 APPLICATION NUMBER: US 08/724,643
7 FILING DATE: 01-OCT-1996
8 ATTORNEY/AGENT INFORMATION:
9 NAME: Apple, Randolph T.
10 REGISTRATION NUMBER: 36,429
11 REFERENCE/DOCKET NUMBER: 015389-0029330US
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (415) 576-0200
14 TELEFAX: (415) 576-0300
15 INFORMATION FOR SEQ ID NO: 224:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 4015 base pairs
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: cDNA
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: 56..3454
25 OTHER INFORMATION: /product= "hTrrt"
26 /note= "human telomerase reverse
27 transcriptase (hTrrt) catalytic protein
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29 SEQUENCE DESCRIPTION: SEQ ID NO: 224:
30 US-10-053-758-224

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Alignment Scores:

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| Db | 62 | CSGGTCCCGCTGCCGAGCCGTGGGTCCCTGTCGCAGGCCACTACCCCGAGGTGCTG | 121 |
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| Db | 122 | CCGCTGGCCACGTTCTGTCGGCGCTGGGGCCCCAGGGCTGGCGGTGTGCAGCGCGGG | 181 |
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| QY | 85 | ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla | 104 |
| Db | 242 | CSGCGGCCCGCGCGCCCTCCTTCGCGCAGGTGCTCCTGCCTGAAGGAGCTGGTGGCC | 301 |
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| Db | 302 | CGAGTGTCTGACAGAGCTGTGCGACGCGCGGCGGAAGAACGTGTGCGCTTCGGCTTCGGG | 361 |
| QY | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr | 144 |
| Db | 362 | CTGTGGACGGGGCCCGGGGGCCCCCGAGGCCTTCACACACAGCGTGCACGACTAC | 421 |
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| DB | 602 | CAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGAGATCGGAACGGGCC | 661 |
| QY | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| DB | 662 | TGGAACCATAGCGTCAGGAGGCGGGGTCCCTGGGCGCTGCCAGCCCGGGTGGGAGG | 721 |
| QY | 245 | ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla | 264 |
| DB | 722 | AGGCGCGGGGCACTGCCAGCGAAGTCTGCCGTGGCCAAGAGGCCAGCGCTGGCGCT | 781 |
| QY | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| DB | 782 | GCCCTTGAGCGGAGCGACGCCCGTTGGCAGGGGTCTTGGGCCCAACC CGGCACGACG | 841 |
| QY | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla | 304 |
| DB | 842 | CGTGGACCGAGTAGCCGTGTTTCTGTGTGTGTCTACCTGCCAGACCGCCGGAAGCC | 901 |
| QY | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| DB | 902 | ACCTCTTGGAGGTGGCGTCTCTGGCACGGCGCACTCCACCCATCCGTGGGCCGCCAG | 961 |
| QY | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| DB | 962 | CACCACGCGGCCCGCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTCCC | 1021 |
| QY | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| DB | 1022 | CCGCTGTACGCGAGACAAAGCACTTCTCTACTCTCCTCAGCGCAAGGACAGCTGCGG | 1081 |
| QY | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| DB | 1082 | CCCTCTCTCTACTCAGCTCTCTGAGGCCCAGCGCTGACTGGCGCTCGGAGGCTCTGGAG | 1141 |
| QY | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| DB | 1142 | ACCATCTTCTGGGTCCAGCGCCCTGGATGCCAGGACCTCCCGCAGAGTGTGCCCCGCTG | 1201 |
| QY | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
| DB | 1202 | CCCCAGCGCTACTGGCAATACGCGCCCTGTTTCTGGAGCTGCTTGGGAACCAACGCGCAG | 1261 |
| QY | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| DB | 1262 | TGCCCTTACGGGGTGCTCTCAAGACGCACTGCCCGCTCGGAGCTCGCTCACCACGCA | 1321 |
| QY | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluGluAsp | 464 |
| DB | 1322 | GCCGGTGTCTGTGCCCGGGAGAGCCCGAGGGCTCTGTGGCGGCCCGGAGGAGGAGAC | 1381 |
| QY | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| DB | 1382 | ACAGACCCGCTCGCTGTGTGTCAGCTGCTCCGCCACGACAGACGCCCTTGGCAGGTGATC | 1441 |
| QY | 485 | GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| DB | 1442 | GGCTTGTGGGGGCTTGCCTTGGCCGGGCTGTGGCCCCAGGCGCTCTTGGGGCTCCAGGCAC | 1501 |
| QY | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys | 524 |
| DB | 1502 | AACGAAGCCGCTTCTCTCAGAAACACACAGAAGTTCTCTCCTTGGGGAGCATGCGCAAG | 1561 |
| QY | 525 | LeuSerLeuGlnLeuLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 |

Db 1562 CTCTCGCTGAGAGCTGAGCTGGAGATGAGCTGGGACCTGCGCTGGCGCAGG 1621
Qy 545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla 564
Db 1622 AGCCAGGGTGGCTGTGCTCGCGCGCAGAGACCGCTGCGGTGAGGAGATCCTGGCC 1681
Qy 565 LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr 584
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Qy 605 LysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
Db 1802 AAGTTCAAAGCATTTGAATCAGACAGCACTTGAAGAGGCTGAGCTGCGGGAGCTGTGC 1861
Qy 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
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Qy 665 ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
Db 1982 AGAACGTTCGCGCAGAGAAAGAGCGCGAGCGTCTCACCTCGAGGCTGAAGGCACCTGTT 2041
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Qy 705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
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Db 2222 GACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTACTCGTGGCT 2281
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Qy 885 LeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHisAlaLysThr 904
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Db 2642 CTCTCGCTTGGTGGATGATTTCTTGTGGTACACCTCACCTCACCCAGCGAAACC 2701
Qy 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
Db 2702 TTCTCAGGACCTGCTGCTCCAGGTGTCCTTGAGTATGGCTGCGTGGTGAATTCGCGAAG 2761
Qy 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
Db 2762 ACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGGGCTTTGTTCAGATG 2821
Qy 945 ProAlaHisGlyLeuPheProTyrPyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964
Db 2822 CCGGCCACCGCTTATTCCTGCTGGGCGCTGCTGCTGGATACCCGAGCCCTGGAGGTG 2881
Qy 965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984
Db 2882 CAGAGGACCTACTCCAGCTATGCCGAGACCTCCATCAGAGCCAGTCTCACCTTCAACCGC 2941
Qy 985 GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004
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Qy 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
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Qy 1025 LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
Db 3062 AAGATCTCTCTGCTGAGCGGTACAGGTTTTCAGCATGTGCTGTCAGCTCCCATTTTCT 3121
Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
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Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
Db 3182 TGCTACTCCATCTGAAAGCCAGAACGACGAGGATGTCGTGGGGCCAGAGGCGCGCC 3241
Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLysLeu 1104
Db 3242 GGCCCTCTGCGCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTG 3301
Qy 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
Db 3302 ACTCGACACCGCTGACCTACGTGCGCATCTCTGGGGTCACTGAGGAGCCGACGACG 3361
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
Db 3362 CTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCGCAACCCGCA 3421
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
Db 3422 CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451

RESULT 6

US-10-208-243-1
; Sequence 1, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: Response to a Telomerase Antigen
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 4015
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (36)..(3454)
 ; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
 US-10-208-243-1

Alignment Scores:

Pred. No.: 0 Length: 4015
 Score: 6057.00 Matches: 1150
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.64% Indels: 0
 DB: 14 Gaps: 0

US-08-951-733-20 (1-1154) x US-10-208-243-1 (1-4015)

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 Db 2 CAGCGCTGGCTCTGCTGGCAGCTGGGAGCCCTGGCCCGCCGCCGCCCGCGATGCGG 61
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 Db 62 CGCGCTCCCGCTGCCGAGCGGTGGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTG 121
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 Db 242 CGCGCGCCCGCGCGCGCCCTCCCTCCGCCAGGTGTCTGCCTCAAGGAGTGGTGCGC 301
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 QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
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 Db 302 CGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGAAGACGTGTGGCTTCGGCTTCGCG 361
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 Db 362 CTGCTGGACGGGCGCGCGGCGCCCGCGAGGCTTTCACCACCGAGGTGGCGAGCTAC 421
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 Db 422 CTGCCCAACACGGTGACCGAGCGCACTGCGGGGGAGCGGGGCGTGGGGCTGCTGTGGCG 481
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 QY 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
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 QY 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264
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QY 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
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 Db 782 GCCCTTGACCGGAGCGGAGCCCGTGGCAGGGGTCTTGGCCCAACCCGGCAGGACG 841
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 QY 385 ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu 404
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 QY 445 AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluGluAsp 464
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1862 1862 GAAGCAGAGGTTCAGCAGCATCGGAGAGCCAGGCCGCCCTGCTGACGTCACAGACTCCGC 1921
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RESULT 7

US-10-054-295-224

; Sequence 224, Application US/10054295

; Publication No. US20030044953A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. US20030044953A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; Zip: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/054,295

; FILING DATE: 18-Jan-2002

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/854,050

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996


```

:
: ATTORNEY/AGENT INFORMATION:
:
:   NAME: Apple, Randolph T.
:
:   REGISTRATION NUMBER: 36,429
:
:   REFERENCE/DOCKET NUMBER: 015389-0029300US
:
: TELECOMMUNICATION INFORMATION:
:
:   TELEPHONE: (415) 576-0200
:
:   TELEFAX: (415) 576-0300
:
: INFORMATION FOR SEQ ID NO: 224:
:
:   SEQUENCE CHARACTERISTICS:
:
:     LENGTH: 4015 base pairs
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:     TYPE: nucleic acid
:
:     STRANDEDNESS: single
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:     TOPOLOGY: linear
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:     MOLECULE TYPE: cDNA
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:       /note= "human telomerase reverse
:
:         transcriptase (hTfT) catalytic protein
:
:         component"
:
:       SEQUENCE DESCRIPTION: SEQ ID NO: 224:
:
: US-10-054-295-224

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| Alignment Scores: | |
|------------------------|---------|
| Pred. No.: | 0 |
| Score: | 6057.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 99.64% |
| DB: | 14 |
| Length: | 4015 |
| Matches: | 1150 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-08-951-733-20 (1-1154) x US-10-054-295-224 (1-4015)

| | | | |
|----|-----|--|-----|
| QY | 5 | GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro | 24 |
| Db | 2 | CAGCGCTCGCTCTCTCGCACGTGGGAAGCCCTGGCCCGCGCACCCCGCATGCCG | 61 |
| QY | 25 | ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu | 44 |
| Db | 62 | CGCGTCCCCGCTGCCGAGCGCTCGCTCCCTGCTGCAGCCACATACCAGGAGGTGCTG | 121 |
| QY | 45 | ProLeuAlaThrPheValArgLeuGlyProGlnGlyTyrArgLeuValGlnArgGly | 64 |
| Db | 122 | CGCTGGCGCATGCTCGTGGCGCTGGGGCCCCAGGGCTGGCGCTGGTGACAGCGGG | 181 |
| QY | 65 | AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla | 84 |
| Db | 182 | GACCCGGCGGTTCCTCCGCGCTGGTGGCCAGTGCCTGTGTGCTGCTGGACGCA | 241 |
| QY | 85 | ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeuValAla | 104 |
| Db | 242 | CGCGCGCCCCCGCGGCCCTCTCTCGCCAGGTGCTTGCCTGAAGAGCTGGTGGCC | 301 |
| QY | 105 | ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla | 124 |
| Db | 302 | CGAGTGTGCAGAGCTGTGGAGCGCGCGCGAAGACGTGTGGCTTCGGCTTCGGCG | 361 |
| QY | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr | 144 |
| Db | 362 | CTGTGTGACGGGGCCCGGGGGCCCCCGAGCGCTTACACACAGCTGCGAGCTAC | 421 |
| QY | 145 | LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg | 164 |
| Db | 422 | CTGCCACACAGGTGACGACCGCACTCGGGGGAGCGGGGGCTGTGTGCTGGCGC | 481 |
| QY | 165 | ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal | 184 |
| Db | 482 | CGCTGGCGCAGCAGCTGCTGTTCCTCTGTCGACGCTGCGGCTCTTGTGTGGTGG | 541 |
| QY | 185 | AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr | 204 |
| Db | 542 | GCTCCAGCTGCGCTTACAGGTGTGGGGCCCGCTGTACAGCTGCGCGCTGCGACT | 601 |


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QY 505 AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys 524
DB 1502 AACGAACGCGCTTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGGAAGCATGCCAAG 1561
QY 525 LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg 544
DB 1562 CTTCTCGCTGCAGAGCTGACGTGGGAAGATGACGTCGGGACTGCGCTTGGCTGCCACG 1621
QY 545 SerProGlyValGlyCysValProAlaGluHisArgLeuArgGluGluLeuAla 564
DB 1622 AGCCAGGGGTGGCTGTCTTCGGCGCCGAGACACCGCTCGTGGAGAGATCCCTGGCC 1681
QY 565 LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr 584
DB 1682 AAGTTCTCATCTGGCTGATGAGTGTACGTGCGAGCTGCTCAGGCTCTTCTTTTAT 1741
QY 585 ValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604
DB 1742 GTCACGGACACCGTTTCAAGAACACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGC 1801
QY 605 LysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
DB 1802 AAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTCG 1861
QY 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
DB 1862 GAAGCAGAGGTGAGGCAGCATCGGAAGCAGCGCGCGCTCTGACGTCCAGACTCCGC 1921
QY 645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664
DB 1922 TTCATCCCCAAGCCTGACGGGCTGGCGCGATGTGGAACATGACGTACGTCTGGGAGCC 1981
QY 665 ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
DB 1982 AGAAGCTTCCGACAGAAAAAGAGGCGCGAGCGTCTCACCTCGAGGTGAAGCAGCTGTC 2041
QY 685 SerValLeuAsnTyrGluAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704
DB 2042 AGCGTGCTCACTACAGCGGCGCGCGCGCGCGCTCTGGCGGCTCTGTGTGGCG 2101
QY 705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
DB 2102 CTGGAGATATCCACAGGCGCTGGCGCACCTTCGTGCTCGTGGCGGCCAGGACCG 2161
QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
DB 2162 CGGCTGTAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCAG 2221
QY 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764
DB 2222 GACAGGCTCAGGAGTCTATCGCCAGCATCAAAACCCAGAACACGTACTGCGTGGCT 2281
QY 765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
DB 2282 CGSTATCGGTGTCAGAAAGCCGCCATGGCAGCTCCGCAAGGCTTCAAGAGCCAC 2341
QY 785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804
DB 2342 GTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG 2401
QY 805 ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer 824
DB 2402 ACCAGCCGCTGAGGATCCGTCGTCATCGAGACAGAGCTCTCCCTGAATGAGGCGAGC 2461
QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
DB 2462 AGTGGCTCTTCGACGCTCTCTACGCTTCATGTGCCACACCGCGCTGGCATCAGGGGC 2521
QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
DB 2522 AAGTCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTCTGC 2581
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QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
DB 2582 AGCTTGTTGTCAGCGGCATCGAGAACAAAGCTGTTTTGCGGGGATTGCGGGGAGGCTG 2641
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
DB 2642 CTTCTGCGTGGTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCGGCAAAACC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
DB 2702 TTCTCTCAGGACCTGTCGAGGTGCTCCAGTATGCTGATGCTGCTGGAACCTTGCGGAAG 2761
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyClyThrAlaPheValGlnMet 944
DB 2762 ACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGCAGCGCTTTGTTCAGATG 2821
QY 945 ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964
DB 2822 CCGGCCCCACGGCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGACCTTGAGGCTG 2881
QY 965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984
DB 2882 CAGAGCGACTACTCCAGCTATGCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCGC 2941
QY 985 GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004
DB 2942 GGTCTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGCTCTTGGGCTGNAAGTGT 3001
QY 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
DB 3002 CACAGCGCTTCTTGGATTTGCAAGTGAACAGCTCCAGCGGTGCACCAACATCTAC 3061
QY 1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
DB 3062 AAGATCTCTCTGTCGAGCGGTACAGGTTTCACGCATGTGTGTCGAGCTCCCATTTTCAT 3121
QY 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
DB 3122 CAGCAAGTTTGAAGAACCCACATTTTCTCGCGCTCATCTCTGACAGCGCTCCCTC 3181
QY 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
DB 3182 TGCTACTCCATCTCTGAAGCCAAAGACGAGGATGCTGCTGGGGCCAAAGGCGCGCC 3241
QY 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLysLeu 1104
DB 3242 GGCGCTCTCGCTCCGAGGCGGTGCAGTGGCTGTGCGCACCAAGCATTCCTGCTCAAGCTG 3301
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DB 3302 ACTCGACACCGTGTACCTACGTACGTCCTCTGGGTCTACTAGGACAGCCCCAGAGCAG 3361
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DB 3362 CTGAGTCGGAAGCTCCCGGGGAGGACGCTGACTGCCCTGGAGGCCGAGCCACCGGCA 3421
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RESULT 9

US-10-105-963-1

; Sequence 1, Application US/10105963

; Publication No. US20030068818A1

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

; APPLICANT: Denning, Chris

; APPLICANT: Clark, A. John

; APPLICANT: Schiiff, J. Michael

; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human

; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst

; TITLE OF INVENTION: Recombination

; FILE REFERENCE: 731/002

; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 14 Gaps: 0

US-08-951-733-20 (1-1154) x US-10-105-963-1 (1-4015)

| | | | |
|----|-----|---|-----|
| Qy | 5 | GlnArgCysValLeuLeuArgThrpGluAlaLeuAlaProAlaThrpAlaMetPro | 24 |
| Db | 2 | CAGCGCTGCGTCCGTCGCGCACGTGGGAAGCCCTGGCCCGGCACCCCGCGATGCG | 61 |
| Qy | 25 | ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu | 44 |
| Db | 62 | CGCGCTCCCGCTGCCGAGCGTGGCTCCCTGCTGCGACGCCACTACCGCGAGGTGCTG | 121 |
| Qy | 45 | ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly | 64 |
| Db | 122 | CCGCTGGCCAGCTTCGTGGCGGCTGGGGCCCGAGGCTGGCGTGGTGGTGGTGGTGG | 181 |
| Qy | 65 | AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla | 84 |
| Db | 182 | GACCGCGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGGTGGTGGTGGTGGTGG | 241 |
| Qy | 85 | ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla | 104 |
| Db | 242 | CGGCG | 301 |
| Qy | 105 | ArgValLeuGlnArgLeuCysGluArgGlyValAlaLysAsnValLeuAlaPheGlyPheAla | 124 |
| Db | 302 | CGAGTGTGTGAGAGCTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 361 |
| Qy | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr | 144 |
| Db | 362 | CTGTGGAGCGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 421 |
| Qy | 145 | LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg | 164 |
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| Qy | 165 | ArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal | 184 |
| Db | 482 | CGGCTGGCGGACGACGTGCTGGTTCACCTGCTGGCAGCGCTGGCGCTTCTTGTGGTG | 541 |
| Qy | 185 | AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr | 204 |
| Db | 542 | GCTCCAGCTGCGCCTACCAAGTGTGGGGCGCGCGCGCTGTACCAAGCTCGCGCTGCC | 601 |
| Qy | 205 | GlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla | 224 |
| Db | 602 | CAGCG | 661 |
| Qy | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| Db | 662 | TGGACCAATACGCTCAGGAGCGCGGGTCCCGCTGGCGCTGCCACCGCGGGTGGGAGG | 721 |

| | | | |
|----|------|---|------|
| Qy | 245 | ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla | 264 |
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| Qy | 265 | AlaProGluProGluArgThrpProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| Db | 782 | GCCCTTGAGCGGAGCGGACGCCCTTGGGAGGGGTCTGGGCCACCGCGGAGGAGG | 841 |
| Qy | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaAatgProAlaGluAla | 304 |
| Db | 842 | GTGAGCCGAGTGACCGTGGTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 901 |
| Qy | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
| Db | 902 | ACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCACCCACTCGTGGCGCCG | 961 |
| Qy | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| Db | 962 | CACCACGCGGCGCGCCCATCCACATCGCGGCGCACACGCTCCCTGGGACACGCTTGT | 1021 |
| Qy | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| Db | 1022 | CCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGCGGCAAGGACGAGTGGG | 1081 |
| Qy | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| Db | 1082 | CCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT | 1141 |
| Qy | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| Db | 1142 | ACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT | 1201 |
| Qy | 405 | ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCGAGCGCTACTGGCAATCGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT | 1261 |
| Qy | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCTTACGGGTGCTCTCAAGACGACCTGCCCGTGGCGTGGCGTGGCGTGGCGTGG | 1321 |
| Qy | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluGluAsp | 464 |
| Db | 1322 | GCCGCTGTCTGTGCGGGAGAGCCCGAGGCTGTGTGGGGGCGCGCGAGGAGGAG | 1381 |
| Qy | 465 | ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr | 484 |
| Db | 1382 | ACAGCCCCCTGCGCTGGTGTGCTCCCGCACACAGCAGCCCCCTGGCAGGTGTAC | 1441 |
| Qy | 485 | GlyPheValArgAlaCysLeuArgLeuValProProGlyLeuTrpGlySerArgHis | 504 |
| Db | 1442 | GGCTTCTGCGGGCTGCTGCTGCGCGGCTGTGTGCGCGCGCGCGCGCGCGCGCGCG | 1501 |
| Qy | 505 | AsnGluArgArgPheLeuArgAsnThrLysLysPheLeSerLeuGlyLysHisAlaLys | 524 |
| Db | 1502 | AACGAACGCGCTTCTCTCAGAACACCAAGAGTTCTATCTCCCTGGGGAACATGCCA | 1561 |
| Qy | 525 | LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg | 544 |
| Db | 1562 | CTCTCGCTGAGGAGCTGACGTGGAGATGAGCTGGGGGACTGCGCTTGGCTGCGCAGG | 1621 |
| Qy | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla | 564 |
| Db | 1622 | AGCCAGGGGTGGCTGTCTGCTGCGCGCGCAGACCGCTGTGCGTGAGGAGATCCTGCC | 1681 |
| Qy | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr | 584 |
| Db | 1682 | AACTTCTGCACTGGCTGATGAGTGTGTAGCTGTGCTGAGTGTGCTGAGTCTTTCTTT | 1741 |
| Qy | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTyrSer | 604 |
| Db | 1742 | GTCACGAGGACGAGCTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGAGC | 1801 |

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605 QY LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
1802 Db AGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTCAGCTGGGAGGTGTGC 1861
625 QY GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
1862 Db GAAGCAGAGGTTCAGGCAGCATCGGAAGCAGCGCCGCTGTCAGCTCCAGACTCCGC 1921
645 QY PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664
1922 Db TTTCATCCCAAGCCCTGACGGGTGCGCGCATTTGTGAACATGACTACGTCTGCGGAGCC 1981
665 QY ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
1982 Db AGNAGCTCCGAGAGAAAAGAGGCGGAGCGCTCTACCTCGAGGGTGAAGCAGCTGTC 2041
685 QY SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerValLeuGly 704
2042 Db AGCGTGCTCACTACGAGGGCGCGCGCCGCTCTGCGGCCCTCTGTGTGGGC 2101
705 QY LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
2102 Db CTGGACGATATCCAGGGCCCTGGCGCACTTCTGCTGCTGCGTGTGCGGCCAGGACCGC 2161
725 QY ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
2162 Db CGCCTGACGTACTTTGTAAGGTGGATGTGACGGGCGGTACGACACCATCCCGCC 2221
745 QY AspArgLeuThrGluValIleAlaSerIleLeuLysProGlnAsnThrTyrCysValArg 764
2222 Db GACAGGCTCAGGAGGTATCGCCAGCATCATCAACCCAGAACACGTACTGCGTGGCT 2281
765 QY ArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
2282 Db CGGTATGCGGTGTCCAGAAGCCGCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCAC 2341
785 QY ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804
2342 Db GTCTCTACCTTCACAGACCTCCAGCGGTACATGCCAGTTCGTGGCTCACCTGAGGAG 2401
805 QY ThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGluAlaSer 824
2402 Db ACCAGCCCGCTCAGGAGTCCGCTCGTCATCGAGCAGAGCTCTCCCTGAATCAGGCGCAGC 2461
825 QY SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844
2462 Db AGTGGCCCTTCGACGCTCTCTCTACGCTTCATGTGCCACACGCGGTGCGCATCAGGGC 2521
845 QY LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
2522 Db AAGTCTACGTCCAGTCCAGGGGATCCGCGAGGGCTCCATCTCTCCACGCTGCTCTGC 2581
865 QY SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
2582 Db ASCCTGTGCTACGGCGACATGAGAACAGCTGTTGCGGGATTCGCGGGACGGGCTG 2641
885 QY LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
2642 Db CTCTCTGCGTTCGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCCACGCAAAACC 2701
905 QY PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
2702 Db TTCTCTCAGACCCCTGGTCGAGGTGTCCGTGAGTATGGCTGGGTGAACCTGGCGAAG 2761
925 QY ThrValValAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheValGlnMet 944
2762 Db ACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCTAGATG 2821
945 QY ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964
2822 Db CGGGCCCAAGCGCTATTCCTCTGGTGGCGCCCTGCTGTGGATACCCGGACCCCTGGAGGTG 2881
965 QY GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984
2882 Db CAGAGCGACTACTCCAGCTATGCCGAGGACTTCCATCAGAGCCAGTCTCACCTTCAACCGC 2941
985 QY GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004
2942 Db GGCTTCAAGCTGGGAGGAACATGCGTCGCAACTCTTTGGGTCTTGGGCTGAAGTGT 3001
1005 QY HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
3002 Db CACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTAC 3061
1025 QY LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
3062 Db AGATCTCTCTGCTGCGAGCGGTACAGGTTTACGCAATGTGTGTCGAGCTCCCATTTTCA 3121
1045 QY GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
3122 Db CAGCAAGTTTGAAGAAGCCACATTTTCTGCGGCTCATCTCTCACAGGCGCTCCCTC 3181
1065 QY CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
3182 Db TGTACTCTCATCTCTCAAGCCAGAACGAGGATGCTGCTGGGGCCCAAGGCGCGCC 3241
1085 QY GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
3242 Db GGCCCTCTCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTG 3301
1105 QY ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
3302 Db ACTCGACACCGGTTCACCTACGTGCGCACCTCTGCGGTCACTCAGGACGCCAGAGCGAG 3361
1125 QY LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsnProAla 1144
3362 Db CTGAGTCGGAAGCTCCCGGGGACGAGCTGACTGCTGGAGCGCCGAGCAACCCGGCA 3421
1145 QY LeuProSerAspPheLysThrIleLeuAsp 1154
3422 Db CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451

RESULT 10
US-10-044-692-1
; Sequence 1, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/044,692
; APPLICATION NUMBER: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
```

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1  APPLICATION NUMBER: US 08/854,050
2  FILING DATE: 09-MAY-1997
3  APPLICATION NUMBER: US 08/851,843
4  FILING DATE: 06-MAY-1997
5  APPLICATION NUMBER: US 08/846,017
6  FILING DATE: 25-APR-1997
7  APPLICATION NUMBER: US 08/844,419
8  FILING DATE: 18-APR-1997
9  APPLICATION NUMBER: US 08/734,643
10 FILING DATE: 01-OCT-1996
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Apple, Randolph T.
13 REGISTRATION NUMBER: 36,429
14 REFERENCE/DOCKET NUMBER: 015389-0026000US
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (415) 576-0200
17 TELEFAX: (415) 576-0300
18 INFORMATION FOR SEQ ID NO: 1:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 4015 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: cDNA
25 FEATURE:
26 NAME/KEY: CDS
27 LOCATION: 56..3454
28 OTHER INFORMATION: /product= "hTfT"
29 /note= "human telomerase reverse
30 transcriptase (hTfT) catalytic protein
31 component"
32 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
33
34 US-10-044-692-1

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| Alignment Scores: | |
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| Pred. No.: | 0 |
| Score: | 6057.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 99.64% |
| DB: | 14 |
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| Matches: | 1150 |
| Conservative: | 0 |
| Mismatches: | 0 |
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US-08-951-733-20 (1-1154) x US-10-044-692-1 (1-4015)

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| QY | 5 | GlnArgCysValLeuLeuAthrTrpGluAlaLeuAlaProAlaThrProAlaMetPro | 24 |
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| QY | 25 | ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu | 44 |
| Db | 62 | CGCGTCCCGCTGCCAGCGTCGCTCCCTGCTGCAGCCACCTACCGCGAGTGCTG | 121 |
| QY | 45 | ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyThrArgLeuValGlnArgGly | 64 |
| Db | 122 | CCGCTGGCCACGTCGTGCGCGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCCGG | 181 |
| QY | 65 | AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla | 84 |
| Db | 182 | GNACCGGGGGCTTCCGGCGCGCTGGTGCCCGAGTGCCTGCTGCGTGCCTGGGACGCA | 241 |
| QY | 85 | ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla | 104 |
| Db | 242 | CGGCGCGCCCCCGCGGCCCTCCTTCGCCAGGTGCTGCCTGAAGAGCTGGTGGCC | 301 |
| QY | 105 | ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla | 124 |
| Db | 302 | CGAGTGTGCAAGAGCTGTGGCAGCGGGCGGAAGAACGTGCTGGCTTCGGCTTCGGCG | 361 |
| QY | 125 | LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr | 144 |
| Db | 362 | CTGTGTGACGGGGCGGGGGGGCCCCCGAGGCGCTTCACACACAGCGTGGCGACGTAC | 421 |
| QY | 145 | LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrPglyLeuLeuLeuArg | 164 |

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| Db | 482 | CGCGTGGCGACGACAGCTGCTGGTTACCTGCTGGCACGCTGCGCGCTCTTTGTGTGGTGG | 541 |
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| Db | 542 | GCTCCAGCTCGCGCTACCAAGTGTGCGGGCGCGCTGTACCAAGTCTGGCGCTGCCACT | 601 |
| Qy | 205 | GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla | 224 |
| Db | 602 | CAGCGCGGGCCCGCCACACCGCTAGTGGACCCCGAAGCGCTGTGGGATGCGAACGGGCC | 661 |
| Qy | 225 | TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg | 244 |
| Db | 662 | TGGAACCATACGCTCAGGGAGCGGGGTCCCTTGGGCTGTCCAGCCCGGGGTGCGAGG | 721 |
| Qy | 245 | ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla | 264 |
| Db | 722 | AGGCGGGGGCAGTGCACGCCGAAGTCTGCGTTGCCAAGAGGCCACGGCGTGGCGCT | 781 |
| Qy | 265 | AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr | 284 |
| Db | 782 | GCCCTTGAGCGCGAGCGGACCCCGTGGGCGAGGGTCTCTGGGCGCCACCCGGCAGGACG | 841 |
| Qy | 285 | ArgGlyProSerAspArgGlyPheCysValValSerProAlaAlaArgProAlaGluAla | 304 |
| Db | 842 | CGTGGACCGAGTGACCGTGGTTCGTGTGTGTGCACGTGCCACACCGCGCGAAGAGCC | 901 |
| Qy | 305 | ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln | 324 |
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| Qy | 325 | HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro | 344 |
| Db | 962 | CACCACGGGGCCCCCATCCACATCGGGGCCACACAGTCCCTGGGACACGCGCTGTGCC | 1021 |
| Qy | 345 | ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg | 364 |
| Db | 1022 | CCGGTGTCGCGCGAGACCAAGCACTCTCTACCTCTCAGCGCAACAAGGACAGCTGCGG | 1081 |
| Qy | 365 | ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu | 384 |
| Db | 1082 | CCCTCTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTGGGAGGCTCGTGGAG | 1141 |
| Qy | 385 | ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu | 404 |
| Db | 1142 | ACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCGAGGTTGCCCGCGCTG | 1201 |
| Qy | 405 | ProGlnArgTyrTrpGlnMetArgProPheLeuGluLeuLeuGlyAsnHisAlaGln | 424 |
| Db | 1202 | CCCCAGCGCTACTGGCAAAATGCGGCCCTGTTCCTGGAGCTGCTTGGGAACACGCGCAG | 1261 |
| Qy | 425 | CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla | 444 |
| Db | 1262 | TGCCCTACGGGTGCTCCTCAAGACGCACTGCCCGTGGCGAGTGGGTCAACCCACGA | 1321 |
| Qy | 445 | AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp | 464 |
| Db | 1322 | GCCGGTCTCTGTGCCGGGAGAGCCCGCGGCTCTGTGGCGGCCCGCAGGAGGAGGAC | 1381 |
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| Db | 1382 | ACAGACCCCGTGGCTGGTGGAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTAC | 1441 |
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| Db | 1442 | GGCTTGTCGGGGCTCCCTGCGCGCGCTGGTGGCCCCAGGCGCTCTGGGGCTCCAGCGAC | 1501 |
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| Db | 1562 | CTCTCGCTGCAGGAGTGCAGTGGAAAGATGAGCGTGCAGGACTGCGCTTGGCTGCAGG | 1621 |
| QY | 545 | SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla | 564 |
| Db | 1622 | AGCCCAAGGGTTGGCTGTCTCGCGCCGAGACCGCTTGGCTGAGGAGATCCTGGCC | 1681 |
| QY | 565 | LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr | 584 |
| Db | 1682 | AACTTCTGCACTGGCTGATGAGTGATGAGTGTACGCTGCGAGTGTCTAGGCTTTCTTTAT | 1741 |
| QY | 585 | ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer | 604 |
| Db | 1742 | GTCAAGGAGACCACTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGGAGC | 1801 |
| QY | 605 | LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer | 624 |
| Db | 1802 | AACTTCAAGCAATTTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTGC | 1861 |
| QY | 625 | GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg | 644 |
| Db | 1862 | GAAGCAGAGTCAAGCAGCATCGGAAGCCAGGCCCGCTGCTGAGCTCCAGACTCCGC | 1921 |
| QY | 645 | PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla | 664 |
| Db | 1922 | TTTCATCCCAAGCCTGACGGCTGCGCGCGATTTGTGAACATGACTACGTCGTGGAGCC | 1981 |
| QY | 665 | ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe | 684 |
| Db | 1982 | AGAACGTTCCGAGAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGTGAAGGCACCTGTC | 2041 |
| QY | 685 | SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly | 704 |
| Db | 2042 | AGCGTCTCAACTACGAGCGGGCGGCGCGCCGCTCTCGGGCCCTCTGTGCTGGCC | 2101 |
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| Db | 2162 | CCGCTGAGCTGTACTTTGTCAAGTGGATGTACGGGCGGTACCGACACCATCCCCCAG | 2221 |
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| QY | 765 | ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis | 784 |
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| QY | 805 | ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer | 824 |
| Db | 2402 | ACCAGCCCGTGAAGGATCCGCTGTCATCGACACAGCTCTCTCCCTGAATGAGGCCAGC | 2461 |
| QY | 825 | SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly | 844 |
| Db | 2462 | AGTGGCTCTCTCGACGCTCTCTTACGCTTCATGTGCACACCGCTGCGCATCAGGGCC | 2521 |
| QY | 845 | LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys | 864 |
| Db | 2522 | AACTCTACGTTCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCAGCTGTCTGC | 2581 |
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| Db | 2582 | AGCTGTGTACGCGCACATGGAGAACAGCTGTTTGGCGGGATTCGGGGGAGGGCTG | 2641 |
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| Db | 2762 | ACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTGTTCAGATG | 2821 |
| QY | 945 | ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal | 964 |
| Db | 2822 | CCGGCCACGGCTATTTCCTCGTGGCGCTCTGCTGTGATACCGGACCTCGGAGGTG | 2881 |
| QY | 965 | GlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg | 984 |
| Db | 2882 | CAGAGGACTACTCCAGCTATGCCGACCTCCATCAGACCCAGTCTCACCTTCAACCGC | 2941 |
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| Db | 3062 | AAATCTCTCTGCTGACGGCTACAGTTTACGATGTGTGTGCTGCTGCTGCTGCTGCTGCT | 3121 |
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| QY | 1065 | CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla | 1084 |
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| QY | 1085 | GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu | 1104 |
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| QY | 1125 | LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla | 1144 |
| Db | 3362 | CTGAGTCGGAAGTCCCGGGGACGCTGACTGCTGCTGAGGCGCGCAGCCACCCGCCA | 3421 |
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| US-10-044-539-1 | | | |
| ; Sequence 1, Application US/10044539 | | | |
| ; Publication No. US2003010093A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Cech, Thomas R. | | | |
| ; Lingner, Joachim | | | |
| ; Nakamura, Toru | | | |
| ; Chapman, Karen B. | | | |
| ; Morin, Gregg B. | | | |
| ; Harley, Calvin | | | |
| ; Andrews, William H. | | | |
| ; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND | | | |
| ; THERAPEUTIC METHODS | | | |
| ; NUMBER OF SEQUENCES: 335 | | | |
| ; CORRESPONDENCE ADDRESS: | | | |

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/954,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-0026000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4015 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "hprt"

/note= "human telomerase reverse

transcriptase (hprt) catalytic protein

component"

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-044-539-1

Alignment Scores:

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| Pred. No.: | 0 | Length: | 4015 |
| Score: | 6057.00 | Matches: | 1150 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 99.64% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-08-951-733-20 (1-1154) x US-10-044-539-1 (1-4015)

Qy 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24

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Db 2 CAGCGCTGCGTCTGCTGGCAGCTGGGAGCCCTGGCCCGGGCCACCCCGCGATGCCG 61

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Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44

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Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGlnArgGly 64

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Db 122 CCGGTGCCACGTTCTGTGCGGCGCTGGGGCCCCCAGGGCTGGCGGCTGGTGCACGGCGGG 181

Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyrPaspAla 84

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Db 182 GACCCGGCGGCTTCCGGCGCTGGTGGCCAGTGCCTGGTGGTGGTGGTGGTGGTGGTGG 241

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Qy 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104

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Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124

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Db 302 CGAGTGCTGCAGAGGCTGTGCGAGCGCGCGGCGAAGACGCTGCTGGCTTCGGCTTCGC 361

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Qy 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144

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Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeuLeuArg 164

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Db 422 CTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCTGGGGCTGGTGGTGGC 481

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Qy 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184

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Db 482 CGCGTGGCGCAGCGAGTGTGCTTACCTGTGCGCACGCTGCGCGCTCTTTGTGGTGG 541

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Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204

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Db 542 GCTCCAGCTGGCGTACCAGGTGTGCGGGCGCGCGCTGTACCAGCTCGGGGCTGCCACT 601

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Qy 205 GlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224

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Qy 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244

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Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264

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Db 722 AGGCGGGGGCGAGTGGCCAGCGAGTCTGCGTGGCCAGAGGCCCGCGGCTGGCGCT 781

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Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284

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Db 782 GCCCTGAGCGGAGCGGACGCCCGCTTGGGAGGGGTCTTGGGCGCGCGCGCGCGCGCG 841

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Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304

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Db 842 CGTGACCGAGTGACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901

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Qy 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324

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Db 902 ACCTCTTTGGAGGGTGGCTCTCTGCGACGGCGCGCGCGCGCGCGCGCGCGCGCGCG 961

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Qy 325 HisHisAlaGlyProProSerThrSerArgProProArgProTyrPaspThrProCysPro 344

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Db 962 CACCACGGGGCG 1021

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Qy 345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364

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Db 1022 CCGGTGTACCGCGAGACCAAGCACTCTCTACTCTCCTCAGGCGCAGCAAGGAGCAGCTGG 1081

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Qy 365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384

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Qy 385 ThrLePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuProArgLeu 404

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Db 1142 ACCATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGGACTCCCGCGAGGTTGCCCGCGCTG 1201

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Qy 405 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln 424

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Db 1202 CCCAGCGCTACTGGCAAACTGGGCGCTGTCTTCTGTGGAGCTGCTTTGGGAACACCGCGAG 1261

Db 3422 CTGCCCTCAGACTTCAAGACCATCTGGAC 3451

RESULT 12

US-09-749-728B-32

; Sequence 32, Application US/09749728B

; Patent No. US20020142457A1

; GENERAL INFORMATION:

; APPLICANT: Umezawa, Akihiro

; APPLICANT: Hata, Jun-ichi

; APPLICANT: Fukuda, Keiichi

; APPLICANT: Ogawa, Satoshi

; APPLICANT: Sakurada, Kazuhiro

; APPLICANT: Gojo, Satoshi

; APPLICANT: Yanada, Yoji

; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES

; FILE REFERENCE: 00766.000043

; CURRENT APPLICATION NUMBER: US/09749,728B

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: H11-372826

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: PCT-JP00-01148

; PRIOR FILING DATE: 2000-02-28

; PRIOR APPLICATION NUMBER: PCT-JP00-07741

; PRIOR FILING DATE: 2000-11-02

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: PatentIn Ver.2.0

; SEQ ID NO 32

; LENGTH: 3396

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; OTHER INFORMATION: (1)...(3399)

US-09-749-728B-32

Alignment Scores:

Pred. No.: 0 Length: 3396

Score: 5961.00 Matches: 1132

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.06% Indels: 0

DB: 10 Gaps: 0

US-08-951-733-20 (1-1154) x US-09-749-728B-32 (1-3396)

Qy 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42

Db 1 ATGCCGCGCGCTCCCGCTCCGAGCGTGGCTCCCTGCTGGCGACCCACTACCGCGAG 60

Qy 43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTyrArgLeuValGln 62

Db 61 GTGCTGCGCTGGCCAGCTTCGTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCG 120

Qy 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValProTyr 82

Db 121 CGCGGGGACCGCGCGCTTCGCGCGCTGGTGGCGCGCTGGTGGCGCGCTGGTGGCGCGCTGG 180

Qy 83 AspaAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuGluLeu 102

Db 181 GAGCGACGGCG 240

Qy 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaValAlaGlnCysLeuValPheGly 122

Db 241 GTGGCGCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

Qy 123 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 142

Db 301 TTGCGCGTGTGACAGGGGGCGCGGGGGCGCGGGGGCGCGGGGGCGCGGGGGCGCGGGGG 360

Qy 143 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrPglyLeuLeu 162

Db 361 AGCTACTGCGCCCAACACGGGTGACCGACGCTCGGGGGGAGCGGGGGGCGGGGGGCGGGG 420

Qy 163 LeuArgArgValGlyAspValLeuValHisLeuLeuAlaAlaArgCysAlaLeuPheVal 182

Db 421 CTGCGCGCGCTGGCGAGCAGCTGCTGGTTCACCTGCTGGCAGCTGGCGCTCTTTGTG 480

Qy 183 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 202

Db 481 CTGGTGGCTCCAGCTGCGCTACCAAGTGTGCGGGCGCGCGCTGTACCAAGTGGCGCT 540

Qy 203 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgArgLeuGlyCysGlu 222

Db 541 GCCACTAGCG 600

Qy 223 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 242

Db 601 CGGGCTGGAACCTAGCTCAGGAGCGCGGGTTCCTGGGCTGCCAGCCCGCGGT 660

Qy 243 AlaArgArgGlyGlySerAlaSerArgSerLeuProLeuProGlyArgProArgArg 262

Db 661 GCGAGGAGCGCGGGGCGAGTCCAGCGCAAGTCTGCGGTTCGCCAAGAGGCCAGCGCT 720

Qy 263 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 282

Db 721 GGCCTGCCCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780

Qy 283 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 302

Db 781 AGGACGCGTGGACCGAGTGACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840

Qy 303 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 322

Db 841 GAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCAGCGCGCTCCCTGCCAGCCCTCCGCTGG 900

Qy 323 ArgGlnHisAlaGlyProProSerThrSerArgProArgProArgProTyrAspThrPro 342

Db 901 CGCCAGCACACCG 960

Qy 343 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 362

Db 961 TGTCGCCGCGTGTACGCGAGACCAAGCAGTCTCTACTCTCCTCAGGCGACAGAGGAGCAG 1020

Qy 363 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 382

Db 1021 CTGGCGCGCTCCCTCTACTCAGCTCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080

Qy 383 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 402

Db 1081 GTGAGACCACTCTTCTGGGTTCAGGCGCTGGATGCCAGGAGTCTCCCGCAGGTGGCC 1140

Qy 403 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHis 422

Db 1141 CGCCTGCCCGACGCGCTACTGGCAATGCGCGCGCTGTCTTCTGGAGCTGTCTGGGAGCCAC 1200

Qy 423 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 442

Db 1201 GCGCAGTGGCGCTACGGGGGTCTCTCAAGACGACGTGCCGCTGCCAGCTGGCGGTCA 1260

Qy 443 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 462

Db 1261 CCAGCAGCGGTGTCTGTGGCGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320

Qy 463 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 482

Db 1321 GAGGACACAGACCGCGCTGGTGCAGCTGTCTGCCCGACGACGACGACGACGACGACGACG 1380

Qy 483 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 502

Db 1381 GTGTACGGCTTCGTGGCGGGCTGTCTGCGCGCGGTGGTGGCGCGCGCGCGCGCGCGCG 1440

Qy 503 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 522

Db 1441 AGGCAACACGACCGCGCTCTCTCAGGAACACCAAGAGGTTCATCTCCCTGGGAGGAT 1500

Qy 523 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTyrLeu 542

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1501 1501 GCCAACTCTCGCTGAGGAGCTGAGCTGGAGATGAGCGTGGGAGCTGCGCTGGCTG 1560
QY 543 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluile 562
Db 1561 CGCAGGAGCCAGGGGTGGCTGTGTTCGGGCCGACAGACCGCTGCTGGTGGAGATC 1620
QY 563 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 582
Db 1621 CTGGCCAAAGTCTCTGCACATGGGTGAGTGTAGTGTAGTGTAGTGTAGTGTATTC 1680
QY 583 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 602
Db 1681 TTTATGTACGGAGACACAGTTTCAAAAGACAGGCTCTTTTCTACCGGAGAGTGT 1740
QY 603 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 622
Db 1741 TGGAGCAAGTTGCAAGACATTGGAATCAGACAGCACTTGAAGAGGGTGCAGTCCGGAG 1800
QY 623 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 642
Db 1801 CTGTGGAGAGAGAGTCAAGGAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGA 1860
QY 643 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 662
Db 1861 CTCGGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGAGACTACGTCGT 1920
QY 663 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 682
Db 1921 GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCGGAGCGTCTCACCTCGAGGGTGAAGGCA 1980
QY 683 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 702
Db 1981 CTGTTCAAGCTGTCAACTACGAGCGGGCGGGCGGCCCGCTCTGGGGCGCTCTGTG 2040
QY 703 LeuGlyLeuAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 722
Db 2041 CTGGGCTGGAGATATCCACAGGGCTTGGCGACCTTCGTGCTGGTGTGGGGCCAG 2100
QY 723 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 742
Db 2101 GACCCGCCCTGAGCTGACTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATC 2160
QY 743 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 762
Db 2161 CCCAGGACAGGCTACGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTACTGC 2220
QY 763 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 782
Db 2221 GTGGCTGCTATGCCGTGTCCAGAAAGCCGCCCATGGGCACGTCCGCAAGGCCITCAG 2280
QY 783 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 802
Db 2281 AGCCAGCTCTACTACCTTGACAGACCTCCAGCGGTACATCGACAGTTCGTGGCTCACCTG 2340
QY 803 GlnGluThrSerProLeuArgAspAlaValValIleGlnLysSerSerLeuAsnGlu 822
Db 2341 CAGGAACAGCCCGCTGAGGATGCCGTGTCATCGACAGAGCTCTCCCTCGAATGAG 2400
QY 823 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 842
Db 2401 GCCAGCAGTGGCTCTCTCGACGCTCTCTACGTTTCATGTGTCACCCACCGCTGGCGATC 2460
QY 843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 862
Db 2461 AGGGGCAAGTCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCGT 2520
QY 863 LeuCysSerLeuCystyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 882
Db 2521 CTCTGACGCTGTGCTACGGCCACATGGAGACAAGCTGTTCGGGGGATTCGGCGGGAC 2580
QY 883 GlyLeuLeuArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAla 902
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2581 2581 GGGCTGCTCTCGCTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCACGCG 2640
QY 903 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 922
Db 2641 AAAACCTTCTCAGGACCTGGTCCAGAGTGTCCCTGAGTATGGCTGCGTGGTGAACATG 2700
QY 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942
Db 2701 CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGCGCTGGGTGGCAGCGCTTGTGT 2760
QY 943 GlnMetProAlaHisGlyLeuPheProTyrPyrCysGlyLeuLeuLeuAspThrArgThrLeu 962
Db 2761 CAGATCCCGGCCACCGCCTATTCCCTGTGGGGCTGCTGCTGTGATACCCGAGCCCTG 2820
QY 963 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 982
Db 2821 GAGGTGCAGAGGACACTTCTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC 2880
QY 983 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 1002
Db 2881 AACCGCGGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTTGGGGTCTTGGCGCTG 2940
QY 1003 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1022
Db 2941 AAGTGTACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTCCACCAAC 3000
QY 1023 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1042
Db 3001 ATCTACAAGATCTCTGCTGTCAGGCGTACAGGTTTACGCAATGTGTGCTGACGCTCCA 3060
QY 1043 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1062
Db 3061 TTTTCATCAGCAGTGTGGAAGAACCCACATTTTCTCGCGCTCATCTCTGACAGCGCC 3120
QY 1063 SerLeuCystyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
Db 3121 TCCCTCTGCTACTCATCTCTGAAGCCAAAGACGAGGATGCTGCTGGGGCCAGAGGC 3180
QY 1083 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1102
Db 3181 GCGCGCGGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGTCACCAAGCATTCCTGCTC 3240
QY 1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122
Db 3241 AAGTGCATCGACACCGCTGTACCTACGTGCGCACTCTGGGGTCACTCAGGACAGCCAG 3300
QY 1123 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1142
Db 3301 ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCGCGCAGCCAC 3360
QY 1143 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1154
Db 3361 CCGGCACTGCCCTCAGACTTCAAGACCATCTCGGAC 3396

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RESULT 13
US-10-205-629-1
; Sequence 1, Application US/10205629
; Publication No. US20030049236A1
; GENERAL INFORMATION:
; APPLICANT: Kassen, Moustapha
; APPLICANT: Jensen, Thomas
; APPLICANT: Rattan, Suresh
; TITLE OF INVENTION: Immortalized Stem Cells
; FILE REFERENCE: 006148.00002
; CURRENT APPLICATION NUMBER: US/10/205,629
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 60/315939
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PA 2001 01148
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

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; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-629-1

Alignment Scores:

Pred. No.: 0 Length: 3453
Score: 5952.00 Matches: 1130
Percent Similarity: 99.91% Conservative: 1
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 97.91% Indels: 0
DB: 14 Gaps: 0

US-08-951-733-20 (1-1154) x US-10-205-629-1 (1-3453)

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Qy 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42
Db 10 ATGCCGCGCGCTCCCGCTCGGAGCGGTGGCTCCCTGCTGCGCAGCCACTACCGCGAG 69
Qy 43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTyrArgLeuValGln 62
Db 70 GTGTGGCGGTGGCGACGTTGTCGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCGAG 129
Qy 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 82
Db 130 CGCGGGAGCCCGCGGCTTCCGCGCGCTGGTGCCCGAGTGCCTGGGTGGGTGCCCTGG 189
Qy 83 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
Db 190 GAGCAGCGCGCCCCCGCGCCCTCTCTCCGCCAGGTGCTCCCTGCTGAAGAGCTG 249
Qy 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 122
Db 250 GTGCCCGAGTGTGTCAGAGCTGTGGAGCGCGCGCGAAGACGTGCTGGCCCTCGGC 309
Qy 123 PheAlaLeuLeuAspGlyAlaArgGlyProGlnAlaPheThrSerValArg 142
Db 310 TTCGCGTGTGGACGGGCGCGCGGGCCCCCGAGGCTTACCCAGCAGCGCTGCGCGCT 369
Qy 143 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrPglyLeuLeu 162
Db 370 AGCTACCTGCCAACACGGTGACCGACGCTGGGGGGAGCGGGCGTGGGGCTGCTG 429
Qy 163 LeuArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 182
Db 430 CTGCCCGCGTGGCGACGACGTCGTGTTTCACTGCTGGCAGCCTGCGCGCTCTTGTG 489
Qy 183 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 202
Db 490 CTGGTGGCTCCAGCTCGGCTACCAAGTGTGGGGCGCGCGCTGTACCAAGCTCGGCGCT 549
Qy 203 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 222
Db 550 GCCACTCAGCGCGCGCGCCACACGCTAGTGACCCCGGAGCGCTCGGGATGCGAA 609
Qy 223 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 242
Db 610 CGGGCTTGAACCATAGCTGAGGAGCGGGGTCCCGCTGGGCTGCCAGCCCGCGGT 669
Qy 243 AlaArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 262
Db 670 GCGAGGAGCGCGGGGAGTGCAGCGCAAGTCTGCCGTGGCCCAAGAGGCCCGAGCGGT 729
Qy 263 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 282
Db 730 GGGCTGCCCTTGAGCGGAGCGAGCGCGCTGGGACAGGGTCTCGGGCCACCCCGGC 789
Qy 283 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 302
Db 790 AGGACGGTGGACCGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 849
Qy 303 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 322
Db 930 GGAGCCAGAGCTTCCCGCAGAGAAAGAGGGCCGAGCGCTCTCACCTCGAGGGTGAAGSCA 1989
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Db 850 GAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCAGCGCCACTCCACCCATCCCGTGGGC 909
Qy 323 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 342
Db 910 CGCAGACACCGCGGGCCCCCATCCACATCGCGGCCACACACGTCCTTGGACACGGCT 969
Qy 343 CysProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 362
Db 970 TGTCCCCGGTGTAGCGCGAGCAAGCACATCTCTACTCTCTCAGGCGACAAGAGGAG 1029
Qy 363 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 382
Db 1030 CTGGGGCCCTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTC 1089
Qy 383 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgLeuPro 402
Db 1090 GTGAGACCACTTCTGGGTTCAGGCCCTGGATGCCAGGACTTCCCGCAGGTTGGCC 1149
Qy 403 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 422
Db 1150 CGCCTGCCCGACGCTACTGGCAATGGCGCCCTGTTTCTGGAGCTGTTGGGAACAC 1209
Qy 423 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 442
Db 1210 GCGAGTGGCCCTACGGGGTGTCTCTCAAGACGACTGCCCGCTGCGAGCTCGGTCACC 1269
Qy 443 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 462
Db 1270 CCAGACGGCGTGTCTGTGCCCGGGAGAACCCAGGGCTCTGTGGCGGGCCCCGAGGAG 1329
Qy 463 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrPgl 482
Db 1330 GAGGACACAGACCCCGCTCGCTGGTGAGCTGTCTCCGCCAGCAGCAGCGCCCTGGCAG 1389
Qy 483 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrPglySer 502
Db 1390 GTGTACGGCTTCGTGGCGGGCTGTCTGCGCGGGTGGTGGCGCCCGCAGGCTCTCGGGCTCC 1449
Qy 503 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 522
Db 1450 AGGCACAACGAACCGCGCTTCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAAGCAT 1509
Qy 523 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 542
Db 1510 GCCAAGCTCTCGCTGCAGAGCTGACGTGAAGATGACCGTGGCGACTGCGCTGGGTG 1569
Qy 543 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 562
Db 1570 GCGAGGAGCCCGAGGGGTGGCTGTGTCCCGCCGAGAGCACCGCTCTGCGTGAGGAGATC 1629
Qy 563 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 582
Db 1630 CTGGCCAAGTTCCTGCAGCTGGCTGATGATGTGTACGTCTGCGAGCTGCTCAGGTCTTTC 1689
Qy 583 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 602
Db 1690 TTTTATGTACGGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTACCGCCCGAGTGTCTC 1749
Qy 603 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 622
Db 1750 TGGAGCAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAG 1809
Qy 623 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 642
Db 1810 CTGTGGAAGCAGAGAGTTCAGGCACATCGGGAACCCAGGCCCGCCCTGCTCAGGTTCAGA 1869
Qy 643 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 662
Db 1870 CTCGCTTCATCCCAAGCCCTGACGGGTGGGGCGGATGTTGTAACATGAGCTACGTCTGTG 1929
Qy 663 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 682
Db 1930 GGAGCCAGAGCTTCCCGCAGAGAAAGAGGGCCGAGCGCTCTCACCTCGAGGGTGAAGSCA 1989
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QY 683 LeuPheSerValLeuAsnThrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 702
Db 1990 CTGTTTCAGCGTGTCAACTACGAGCGGGCGCGCCCGCTCCCTGGCGCCTCTGTG 2049
QY 703 LeuGlyLeuAspIleHisArgAlaTyrPheValLeuArgValArgAlaGln 722
Db 2050 CTGGGCTCGAGATATCCACAGGGCTGGCGACCTTCGTGCTGGTGGGGCCAG 2109
QY 723 AspProProGluLeuThrPheValLysValAspValThrGlyAlaTyrAspThrIle 742
Db 2110 GACCCGCCCTGAGTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACACATC 2169
QY 743 ProGlnAspArgLeuThrGluValIleAlaSerIleIleIysProGlnAsnThrTyrCys 762
Db 2170 CCCAGGACAGGCTCAGGAGGTATCGCCAGCATCATCAACCCAGAACACGTACTGC 2229
QY 763 ValArgArgTyrAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 782
Db 2230 GTGGTGTGATGCGGTGTCCAGAGGCGCCCATGGGCACGTCCGCAAGGCCCTCAAG 2289
QY 783 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 802
Db 2290 AGCCAGCTCTACCTTGACAGACCTCCAGCGGTACATCGACAGTTCGTGGCTCACCTG 2349
QY 803 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGlu 822
Db 2350 CAGGAGACAGCCCGCTGAGGATGCGGTGTCATCGACGACGCTCCCTCGAATGAG 2409
QY 823 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 842
Db 2410 GCCAGCAGTGGCTCTTCAGCTCTTCCTACGCTTCATGTGTCACACCGCGTGCACATC 2469
QY 843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 862
Db 2470 AGGGGCACTCTACGTCCAGTGCCAGGGATCCCGCAGGGTCCATCTCTCCACGCTG 2529
QY 863 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgAsp 882
Db 2530 CTCTGAGGCTGTGCTACGGCAGCATGGAGAACAGCTTTTCGGGGGATTCGGCGGGAC 2589
QY 883 GlyLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 902
Db 2590 GGGCTGCTCTCGGTTTGGTATGATTTCTTGTGTGTCACACCTCACCTCACCGCGG 2649
QY 903 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 922
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QY 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942
Db 2710 CGGAAGACAGTGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTGT 2769
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QY 963 GluValGlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 982
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QY 983 AsnArgGlyPheIysAlaGlyArgAsnMetArgLysLeuPheGlyValLeuArgLeu 1002
Db 2890 AACCGCGGCTTCAAGGCTGGGAGAACATGCGTCCGCAAACTTTTGGGCTCTGCGGGT 2949
QY 1003 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1022
Db 2950 AGTGTACAGGCTGTTCTTGATTTGAGGTGACAGGCTCCAGCAGGTGTGCACCAAC 3009
QY 1023 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1042
Db 3010 ATCTACAAGATCTCTCTGTGAGGCGTACAGTTTCACGGCATGTGTGTGCTGACGCTCCA 3069
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QY 1043 PheHisGlnGloValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1062
Db 3070 TTTTCATCAGCAAGTTTGGAGAACCCACATTTTCTCGCGCTCATCTCTGACACGGCC 3129
QY 1063 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
Db 3130 TCCTCTGTACTCCATCTCTGAAGCCAGAACGAGGATGTCTGCTGGGGCCAGGGC 3189
QY 1083 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1102
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QY 1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122
Db 3250 AGCTGACTCGACACCGCTGTCACGTACGTGCCACTCTGGGGTCACTCAGGACGCCAG 3309
QY 1123 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1142
Db 3310 ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGTGACTGCCCTGGAGGCCGCGCAAC 3369
QY 1143 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1154
Db 3370 CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC 3405

RESULT 14
US-10-105-616-1
; Sequence 1, Application US/10105616
; Publication No. US20030175967A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Clark, A. J.
; APPLICANT: Denning, Chris
; APPLICANT: Cui, Wei
; APPLICANT: Zhao, Debbiao
; TITLE OF INVENTION: Vectors for Telomerizing Nuclear Donor Cells and Improving the
; TITLE OF INVENTION: of Nuclear Transfer
; FILE REFERENCE: 732/002
; CURRENT APPLICATION NUMBER: US/10/105,616
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US Provisional Application 60/277,749
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13766
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial construct comprising human TERT, myeloproliferative
; OTHER INFORMATION: rcoma virus (MPSV) promoter, and vector components
US-10-105-616-1
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Alignment Scores:
Pred. No.: 0 Length: 13766
Score: 5952.00 Matches: 1130
Percent Similarity: 99.91% Conservative: 1
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 97.91% Indels: 0
DB: 12 Gaps: 0
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US-08-951-733-20 (1-1154) x US-10-105-616-1 (1-13766)

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QY 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42
Db 3989 ATGCCGCGCTCCCGCTGCCGAGCGTCCCTGCTGCCAGCAGCCACTACCGCAG 4048
QY 43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGln 62
Db 4049 GTGCTGCCCTGGCCACGTTCGTGGCGGCCCTGGGGCCCCAGGGCTGGGGTGGCAG 4108
QY 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 82
Db 4109 CCGGGGAGACCCCGCGGCTTTCCGCGCGCTGGTGGCCCACTGCTGTGCTGCTGG 4168
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| | | | |
|----|------|---|------|
| QY | 83 | AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu | 102 |
| DB | 4169 | GACGACCGCCGCCCGCCGCCCTTCCTTCGCCAGGTGTCTCTCCCTGAAGAGCGTG | 4228 |
| QY | 103 | VallAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAanValLeuAlaPheGly | 122 |
| DB | 4229 | GTGGCCCGAGTGTCTGACAGAGCTGTGGAGCGCGCGGAAGACGTGCTGGCGCTTCGGC | 4288 |
| QY | 123 | PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluLaLaPheThrThrSerValArg | 142 |
| DB | 4289 | TTCCGCGTGTCTGGACGGGGCCCGCGGGGGCCCCCGAGGCGCTTCACACACAGCGTCGCG | 4348 |
| QY | 143 | SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrGlyLeuLeu | 162 |
| DB | 4349 | AGCTACCTGCCCAACACGGTGACCGACGTGCGGGGGACGCGGGGGCGTGGGGCGTGTG | 4408 |
| QY | 163 | LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal | 182 |
| DB | 4409 | CTGGCGCGGTGGCGAGCGAGTCTGGTTACCTGTCTGGCACGCTCGCGCTCTTTGTG | 4468 |
| QY | 183 | LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla | 202 |
| DB | 4469 | CTGCTGGCTCCACGCTCGGCTACAGGTGTGGGGCGCGCGCTGTACACAGCTCGCGCT | 4528 |
| QY | 203 | AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu | 222 |
| DB | 4529 | GCCACTCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGGAAGGCGTCTGGGATGCGAA | 4588 |
| QY | 223 | ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 242 |
| DB | 4589 | CGGCGCTGGAAACCATAGCTCAGGAGCGCGGGTCCCTCTGGCGCTGCCAGCCCGGGT | 4648 |
| QY | 243 | AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 262 |
| DB | 4649 | GCGAGGAGCGCGGGGCGAGTGCAGCGAAGTCTGCGTGTGCCAAGAGCGCCAGCGCT | 4708 |
| QY | 263 | GlyAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 282 |
| DB | 4709 | GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGGCAGGGGTCTCTGGGCGCCACCGGGC | 4768 |
| QY | 283 | ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu | 302 |
| DB | 4769 | AGGACGCGTGGACCGAGTGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 4828 |
| QY | 303 | GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 322 |
| DB | 4829 | GAAGCCACCTCTTTGGAGGTGCGCTCTCTGGCACCGCGCACCTCCACCCATCCGTGGC | 4888 |
| QY | 323 | ArgGlnHisAlaGlyProProSerThrSerArgProProArgProThrPaspThrPro | 342 |
| DB | 4889 | CGCCAGCACACGGGGCCCCCATTCACATCGCGGCCACACAGTCCCTGGGACACGCGCT | 4948 |
| QY | 343 | CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln | 362 |
| DB | 4949 | TGTCCCGCGGTGTACGCGAGACCAAGCATCTCTACTCTCTCTCTCTCTCTCTCTCTCT | 5008 |
| QY | 363 | LeuArgProSerPheLeuLeuSerLeuArgProSerLeuThrGlyAlaArgArgLeu | 382 |
| DB | 5009 | CTCGCGGCCCT | 5068 |
| QY | 383 | ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro | 402 |
| DB | 5069 | GTGGAGACCATCTTTCTGGGTTCACGGCCCTGGATGCCAGGGACTCCCCCGAGGTGGCC | 5128 |
| QY | 403 | ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHis | 422 |
| DB | 5129 | CGCTCTGCCCGAGCGCTACTGGCAAAATCGGCCCTCTTTCTGGAGCTGTCTTGGGAAC | 5188 |
| QY | 423 | AlaGlnCysProThrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr | 442 |
| DB | 5189 | GCGCAGTGGCCCTACGGGTGTCTCTCAAGACGACTGCCGCTGGAGCTCGGCTGACG | 5248 |

| | | | |
|----|------|--|------|
| QY | 443 | ProAlaAlaGlyValIcYsAlaAArgGluLysProGlnGlySerValAlaAlaProGluGlu | 462 |
| Db | 5249 | CCAGGACGCGGTGTGTGTGCCGGAGAAGCCAGGGCTCTGTGGCGGCCCGCCAGGAG | 5308 |
| QY | 463 | GluAspThrAspProAArgLeuValGlnLeuLeuArgGlnHisSerSerProThrGln | 482 |
| Db | 5309 | GAGGACACAGACCCCGCTGGCTGTGTGAGCTGTCTCGGCCACAGCACAGCCCTTGGCAG | 5368 |
| QY | 483 | ValTyRGlyPheValArgAlaCysLeuAArgLeuValProProGlyLeuTTPGlySer | 502 |
| Db | 5369 | GNGTACGGCTTCGTGCGGGCCCTGCCTGGCCCGGGTGTGTGCCCCAGGCCCTCTGGGGCTCC | 5428 |
| QY | 503 | ArgHisAsnGluAArgPheLeuAArgAsnThrLysLysPheLleSerLeuGlyLysHis | 522 |
| Db | 5429 | AGGCCAACGAACGCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT | 5488 |
| QY | 523 | AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu | 542 |
| Db | 5489 | GCCAAAGCTCTCGCTCGAAGAGCTGACGTGGGAAGATGAGCGTGGCGGACTCGGCTTGCGTG | 5548 |
| QY | 543 | ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuAArgGluGluLe | 562 |
| Db | 5549 | CGCAGGAGCCAGGGTTGGCTGTGTCTCCGGCCCCAGAGCACCGCTCTGCGTAGGAGATC | 5608 |
| QY | 563 | LeuAlaLysPheLeuHisTrpLeuMetSerValTyRValValGluLeuLeuAArgSerPhe | 582 |
| Db | 5609 | CTGGCCAAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCTCGAGCTGCTCAGGTCTTTC | 5668 |
| QY | 583 | PheTyRValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyRArgLysSerVal | 602 |
| Db | 5669 | TTTTATGTACGGAGACACAGCTTTCAAAGAACAAGGCTCTTTTCTACCGCGCCGAGTGTC | 5728 |
| QY | 603 | TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuAArgGlu | 622 |
| Db | 5729 | TGGAGCAAGTTCAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCCGGAG | 5788 |
| QY | 623 | LeuSerGluAlaGluValArgGlnHisArgGluAlaAArgProAlaLeuLeuThrSerArg | 642 |
| Db | 5789 | CTGTGGGAAGCAGAGGTGAGCAGCATCTGGGAAGCCAGGCCGCGCTGCTGACGTCCAGA | 5848 |
| QY | 643 | LeuArgPheIleProLysProAspGlyLeuAArgProIleValAsnMetAspTyRValVal | 662 |
| Db | 5849 | CTCCGCTTCATCCCCAGCCTTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG | 5908 |
| QY | 663 | GlyAlaArgThrPheAArgArgGluLysArgAlaGluAArgLeuThrSerArgValLysAla | 682 |
| Db | 5909 | GGAGCCAGAACTTCCGCAGAGAAAAGAGGGCCGCGGTCTCACCTTCGAGGGTGAAGCCA | 5968 |
| QY | 683 | LeuPheSerValLeuAsnTyRGluAArgAArgProGlyLeuLeuGlyAlaSerVal | 702 |
| Db | 5969 | CTGTTACAGCTGTCTCAACTACGAGCGGGCGCGGCCCTCTCTGGCGGCTCTGTG | 6028 |
| QY | 703 | LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuAArgValArgAlaGln | 722 |
| Db | 6029 | CTGGGCTGGACGATATCCACAGGGCTGCGGCAACCTTGTGTGCTGTGTGGGGGCCAG | 6088 |
| QY | 723 | AspProProGluLeuTyRPhyValLysValAspValThrGlyAlaTyRAspThrIle | 742 |
| Db | 6089 | GACCGCGGCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCATC | 6148 |
| QY | 743 | ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyRys | 762 |
| Db | 6149 | CCCCAGGACAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTACTGC | 6208 |
| QY | 763 | ValArgArgTyRAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys | 782 |
| Db | 6209 | GTGGCTCGGTATGCGGTGGTCCAGAAGGCCGCGCATGGCAGCGTCCGCAAGGCTTCAAG | 6268 |
| QY | 783 | SerHisValSerThrLeuThrAspLeuGlnProTyRMetArgGlnPheValAlaHisLeu | 802 |
| Db | 6269 | AGCCACGCTCTACCTTGACAGACCTCCACGCCGTATCGGACAGTTCGTGGCTCACCTTG | 6328 |
| QY | 803 | GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu | 822 |


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|||||
6329 CAGGAGACAGCCCGCTGAGGATGCCGTCGTCATCGACAGAGCTCCTCCTGATGAG 6388
QY
823 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 842
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6389 GCCAGCAGTGGCGCTCTTCGACGCTCTCTCTACGCTTCATGTGCACACCGCGCTGCGCATC 6448
QY
843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 862
|||||
6449 AGGGGCAAGTCTTACGTCAGGCCAGGGATCCCGCAGGGTCCCATCTCTCCAGCGTG 6508
QY
863 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 882
|||||
6509 CTCTGCAGCCTGTGCTACGCGACATGGAGACAGCTCTTTGCGGGGATTGCGGGGAC 6568
QY
883 GlyLeuLeuLeuArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAla 902
|||||
6569 GGGCTGCTCTCGTGTGGTGATGATTTCTGTTGGTGACACCTCACCTCACCGCGG 6628
QY
903 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValLeuLeu 922
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6629 AAAACCTCTCAGGACCTGTGCGAGGTGTCCTGAGTATGGCTGCGTGTGAACCTTG 6688
QY
923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942
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6689 CGGAAGACAGTGGTGAACCTTCTGTAGAAGACGAGGCCCTGGGTGGCACGCTTTGTT 6748
QY
943 GlnMetProAlaHisGlyLeuPheProTyrPyrCysGlyLeuLeuLeuAspThrArgThrLeu 962
|||||
6749 CAGATGCCGCGGCACCGGCTATTCCTCGTGGCGCTGCTGCGATACCGCGACCGTG 6808
QY
963 GluValGlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 982
|||||
6809 GAGGTGACAGGAGCTACTCCAGCTATGCCCGGACCTCCATCAGACCCAGTGTACCTTC 6868
QY
983 AsnArgGlyPheLysAlaGlyArgAsnMetArgLysLeuPheGlyValLeuArgLeu 1002
|||||
6869 AACCGCGGCTTCAAGGCTGGAGAACATGCGTCGCAAACTCTTGGGCTCTTGGGCTG 6928
QY
1003 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1022
|||||
6929 AAGTGTACAGCCTGTCTTGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC 6988
QY
1023 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1042
|||||
6989 ATCTCAAGATCCTCTGCTGAGCGGTACAGGTTTCACGATGTGTGCTGCAGCTCCCA 7048
QY
1043 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1062
|||||
7049 TTTTCATCAGCAAGTTTGAAGAACCACCATTTTCTCGCGCTCATCTCTCACAGGCC 7108
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1063 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
|||||
7109 TCCTCTGTACTCCTCATCTGTAAGCCAAAGACGAGGATGTCGCTGGGGCCAAAGGCC 7168
QY
1083 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1102
|||||
7169 GCGCGCGGCTCTGCTCTCCAGGCGGTGAGTGCTGTGCCAACATCTCTGTCVC 7228
QY
1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122
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7229 AAGCTGACTCGACACCGTGTACCTACGTGCGACCTCTCTGGGTGCTACTCAGGACGCCAG 7288
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1123 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1142
|||||
7289 ACGCAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCCGCAGCAAC 7348
QY
1143 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1154
|||||
7349 CCGGCACCTGCCCTCAGACTTCAAGACCATCCCTGGAC 7384
|||||
RESULT 15
US-10-105-616-6/c
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; Sequence 6, Application US/10105616
; Publication No. US20030175967A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Clark, A. J.
; APPLICANT: Denning, Chris
; APPLICANT: Cui, Wei
; APPLICANT: Zhao, Debbiao
; TITLE OF INVENTION: Vectors for Telomerizing Nuclear Donor Cells and Improving the
; FILE REFERENCE: 732/002
; CURRENT APPLICATION NUMBER: US/10/105,616
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US Provisional Application 60/277,749
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 8742
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial construct comprising human TERT, myeloproliferative
; US-10-105-616-6
Alignment Scores:
Pred. No.: 0 Length: 8742
Score: 5925.00 Matches: 1129
Percent Similarity: 99.82% Conservative: 1
Best Local Similarity: 99.73% Mismatches: 2
Query Match: 97.47% Indels: 1
DB: 12 Gaps: 0
US-08-951-733-20 (1-1154) x US-10-105-616-6 (1-8742)
QY 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42
Db 5600 ATGCCGCGGCTCCCGCTGCGAGCGCTGCCCTGCCAGCCACTACCCGCGAG 5541
QY 43 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 62
Db 5540 GTGCTGCCGTGGCCACGTTCTGTCGGCGGCTGGGCGCCAGGGCTGGGGCTGGTGAC 5481
QY 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValProTyr 82
Db 5480 CCGCGGGACCCGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGGCTGGCTGG 5421
QY 83 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
Db 5420 GACGACGGCGCGCGCGCGCGCGCGCGCTCTTCCGCGAGGTGCTTCCCTGAAGAGCTG 5361
QY 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 122
Db 5360 GTGGCCGAGTGCTGCAGAGGCTGTGCGAGCGGCGCGAGAACGCTGCTGGCTTCGGC 5301
QY 123 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 142
Db 5300 TTCGCGCTGCTGGACGGCGCGCGGGGCGCGCGCGCGCGCGCTTCCACCGAGCGCTG 5241
QY 143 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 162
Db 5240 AGCTACTCTCCCAACACGCTGACCGACGCTGCGGGGAGCGGGGCGCTGGGCGCTG 5181
QY 163 LeuArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 182
Db 5180 CTGGCGCGCTGGGCGACGACGCTGCTGGTTACCTCTGCGACGCTGCGCGCTCTTGTG 5121
QY 183 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 202
Db 5120 CTGGTGGCTCCCGAGCTGCGCTACCAAGTGTGCGGGCGCGCGCTGTACAGCTCGCGCT 5061
QY 203 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGlu 222
```

| | | | | | | | |
|----|------|---|------|----|------|---|------|
| Db | 5060 | GCCACTCAGGCGCGCCGCCCCGCCACACGCTAGTGGACCCCGAAGCGCGTCTGGGATGCCAA | 5001 | Db | 3980 | CTGGCCAAAGTTCTCTGCACCTGGCTGATGAGTGG-TACGTGCTGAGAGCTGCTCAGGCTCTTTC | 3922 |
| Qy | 223 | ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly | 242 | Qy | 583 | PheTyrValThrGluThrThrpheGlnLysAsnArgLeuPhePheTyrArgLysSerVal | 602 |
| Db | 5000 | CGGCGCTGGAAACCATAGCGTCAGGAGCGCGGGGTCCCCCTGGCGCTGCCAGCCCGGGT | 4941 | Db | 3921 | TTTTATGTCACGGAGACACCGTTTCAAAGAACACAGCGCTCTTTTCTACGGCCGAGTGTTC | 3862 |
| Qy | 243 | AlaArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg | 262 | Qy | 603 | TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu | 622 |
| Db | 4940 | CGGAGGAGCGCGGGGCGAGTGCACAGCGGAAGTCTGCCGTGTGCCAAGAGGCCCGAGCGGT | 4881 | Db | 3861 | TGGAGCAAGTTGCCAAAGCATTTGGAATCAGACAGCAGCTTGAAGAGGGTCAGCTCGGGAG | 3802 |
| Qy | 263 | GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly | 282 | Qy | 623 | LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg | 642 |
| Db | 4880 | GCGCTGCCCCCTGAGCGGAGCGACCGCCGTTGGGAGGGGTCTTGGGCCCGCCCGGGC | 4821 | Db | 3801 | CTGTGGAAGCAGAGGTTCAGGCAGCATCGGAAGCAGCGCGCCGCTCTGCTCAGCTCCAGA | 3742 |
| Qy | 283 | ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaAlaTrpProAlaGlu | 302 | Qy | 643 | LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal | 662 |
| Db | 4820 | AGGAGCGGTGACCGAGTGACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 4761 | Db | 3741 | CTCCGCTTCATCCCAACCCCTGACGGGTGCGCGCGATTTGTGAACATGGATACCTCTGTG | 3682 |
| Qy | 303 | GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly | 322 | Qy | 663 | GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla | 682 |
| Db | 4760 | GAAGCCACCTCTTTGGAGGGTGCCTCTTGGCACGGGCCACTCCACCCATCCGTGGGC | 4701 | Db | 3681 | GGAGCCACAACGTTCCGCAGAGAAAAGAGGCGGAGCGTCTCACCTCGAGGGTGAAGCA | 3622 |
| Qy | 323 | ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro | 342 | Qy | 683 | LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal | 702 |
| Db | 4700 | CGCCAGCACCCAGCGGGCCCCCATCCACATCGCGGCCACACCTCCCTGGGACACGGCT | 4641 | Db | 3621 | CTGTACGCTGCTCACTACAGCGGCGCGCGCGCCCGGCTCTCTGGGCGCTCTGTG | 3562 |
| Qy | 343 | CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln | 362 | Qy | 703 | LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln | 722 |
| Db | 4640 | TGTCGCCCGGTGTACGCGGACCAAGCACTCTCTACTCTCAGGGCACAAAGAGCAG | 4581 | Db | 3561 | CTGGCGCTGGAGGATATCCACAGGGCTTGGCGACCTTCGTGCTGCGTGGGGGCCACG | 3502 |
| Qy | 363 | LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu | 382 | Qy | 723 | AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle | 742 |
| Db | 4580 | CTGGCGCCCTCTCTTCTACTCAGCTCTCAGAGGCCACGCTGACTGGCGCTCGGAGGCTC | 4521 | Db | 3501 | GACCGCGCGCTGAGCTGACTTTGTCAAGTGGATGTGAGGGGCGCTAGCACACCATC | 3442 |
| Qy | 383 | ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro | 402 | Qy | 743 | ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys | 762 |
| Db | 4520 | GTGGAGACCATCTTCTGGGTTCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGTGCC | 4461 | Db | 3441 | CCCAGGACAGGCTCACGGAGGTTCATCGCCAGCTCATCAACCCCGAAGACGCTACGTC | 3382 |
| Qy | 403 | ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis | 422 | Qy | 763 | ValArgTyrTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys | 782 |
| Db | 4460 | CGCCTGCCCGCAGCGCTACTGCAAAATGCGGCCCTCTTCTGGAGCTGCTTGGGACCA | 4401 | Db | 3381 | GTGGCTCGGTATGCGGTGTCCAGAGGCGCGCCCATGGGACGCTCCGCAAGCCCTCAAG | 3322 |
| Qy | 423 | AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr | 442 | Qy | 783 | SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu | 802 |
| Db | 4400 | GCGCAGTGCCTTACGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA | 4341 | Db | 3321 | AGCCACGCTCTACTCTTGCACAGCCTCCAGCGCTACATGCGACAGTTCGTGCTCACCTG | 3262 |
| Qy | 443 | ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu | 462 | Qy | 803 | GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu | 822 |
| Db | 4340 | CCAGCACCGGTGTCTGTGCCGGGAGAGCCCCCAGGGCTCTGTGGCGGCCCGGAGG | 4281 | Db | 3261 | CAGGACCCAGCCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCTCTCCTGAATGAG | 3202 |
| Qy | 463 | GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln | 482 | Qy | 823 | AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle | 842 |
| Db | 4280 | GAGGACACAGACCCCGCTCGCTGGTGCAGCTGCTCGCCACGACACAGCCCTTGCAG | 4221 | Db | 3201 | GCCAGCAGTGGCCCTTTCGACGCTTCTCTAGCTTCATGTGCCACACGCGCTGGCATC | 3142 |
| Qy | 483 | ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer | 502 | Qy | 843 | ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu | 862 |
| Db | 4220 | GTGTACGGCTTCTGTGCGGGCTGCTGCTGCGCGGTGTGTGCCCCCAGGCGCTCTGGGGCTC | 4161 | Db | 3141 | AGGGCAAGTCTCAGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTG | 3082 |
| Qy | 503 | ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis | 522 | Qy | 863 | LeuCysSerLeuCysTyrGlyAspMetLysLysLeuPheAlaGlyIleArgArgasp | 882 |
| Db | 4160 | AGGCACAACGACCGCCCTCTCTCAGGACACCAAGAAAGTTCATCTCCCTGGGGAAGCAT | 4101 | Db | 3081 | CTCTGCGCCCTGTCTACGGCGCATGGAGAACAGCTGTGTGGGGGATTCGCGGGGAC | 3022 |
| Qy | 523 | AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu | 542 | Qy | 883 | GlyLeuLeuLeuArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAla | 902 |
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| Qy | 543 | ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIle | 562 | Qy | 903 | LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu | 922 |
| Db | 4040 | CGCAGGAGCCCGGGGTGGCTGTGTTCGGCGCGCAGAGCACCGCTCTGCGTGGAGGATC | 3981 | Db | 2961 | AAAACCTTCTCAGGACCTGCTCCGAGGTGCTCCTGAGTATGGCTGCTGCTGAACCTG | 2902 |
| Qy | 563 | LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe | 582 | Qy | 923 | ArgLysThrValValAsnPheProValClnAspGluAlaLeuGlyGlyThrAlaPheVal | 942 |
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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SUMMARIES

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| 2 | 3784.4 | 99.6 | 4015 | 10 | US-09-990-080-1 | | Sequence 1, Appli |
| 3 | 3784.4 | 99.6 | 4015 | 10 | US-09-843-676-224 | | Sequence 224, App |
| 4 | 3784.4 | 99.6 | 4015 | 10 | US-09-953-052-1 | | Sequence 1, Appli |
| 5 | 3784.4 | 99.6 | 4015 | 14 | US-10-053-758-224 | | Sequence 224, App |
| 6 | 3784.4 | 99.6 | 4015 | 14 | US-10-208-243-1 | | Sequence 1, Appli |
| 7 | 3784.4 | 99.6 | 4015 | 14 | US-10-054-295-224 | | Sequence 224, App |
| 8 | 3784.4 | 99.6 | 4015 | 14 | US-10-054-611-224 | | Sequence 224, App |
| 9 | 3784.4 | 99.6 | 4015 | 14 | US-10-105-963-1 | | Sequence 1, Appli |
| 10 | 3784.4 | 99.6 | 4015 | 14 | US-10-044-692-1 | | Sequence 1, Appli |
| 11 | 3784.4 | 99.6 | 4015 | 14 | US-10-044-539-1 | | Sequence 1, Appli |
| 12 | 3618.6 | 95.3 | 4029 | 10 | US-09-843-676-173 | | Sequence 173, App |
| 13 | 3618.6 | 95.3 | 4029 | 11 | US-09-438-486-173 | | Sequence 173, App |
| 14 | 3618.6 | 95.3 | 4029 | 11 | US-10-053-758-173 | | Sequence 173, App |
| 15 | 3618.6 | 95.3 | 4029 | 14 | US-10-054-295-173 | | Sequence 173, App |
| 16 | 3618.6 | 95.3 | 4029 | 14 | US-10-054-611-173 | | Sequence 173, App |

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| 17 | 3410.4 | 89.8 | 3855 | 14 | US-10-044-692-4 | Sequence 4, Appl |
| 18 | 3410.4 | 89.8 | 3855 | 14 | US-10-044-539-4 | Sequence 1, Appl |
| 19 | 3400 | 89.5 | 3453 | 14 | US-10-205-629-1 | Sequence 1, Appl |
| 20 | 3400 | 89.5 | 13766 | 12 | US-10-105-616-1 | Sequence 1, Appl |
| 21 | 3396 | 89.4 | 3396 | 10 | US-09-749-728B-32 | Sequence 32, Appl |
| 22 | 3388 | 89.2 | 8742 | 12 | US-10-105-616-6 | Sequence 6, Appl |
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| 24 | 1730.8 | 45.6 | 2176 | 14 | US-10-044-692-3 | Sequence 3, Appl |
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| 27 | 1654.6 | 43.6 | 2171 | 10 | US-09-766-253-100 | Sequence 100, App |
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| 41 | 1270 | 33.4 | 1314 | 14 | US-10-294-778-9 | Sequence 9, Appl |
| 42 | 1254 | 33.0 | 1311 | 14 | US-10-294-778-1 | Sequence 1, Appl |
| 43 | 873 | 23.0 | 873 | 12 | US-10-282-960-1 | Sequence 1, Appl |
| 44 | 519 | 13.7 | 519 | 12 | US-10-282-960-2 | Sequence 2, Appl |
| 45 | 385.8 | 10.2 | 389 | 10 | US-09-843-676-62 | Sequence 62, Appl |

ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
; US-09-733-294A-3

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Query Match          99.6%; Score 3784.4; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| QY | 613 | TCAGGCGCGCCCGCCACACGCTACTGACCCCGGAAGCGGTGGATGCGAAGCGGC | 672 |
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| Db | 661 | CTGGAACATAGCTCAGGAGGCGGGGTCCCGCTGGGCTGCCAGCCCGGGTGGAG | 720 |
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| QY | 1153 | GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCCT | 1212 |
| Db | 1141 | GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCCT | 1200 |
| QY | 1213 | GCCCCAGCGTACTTGGCAATGCGGGCCCTGTTTCTGGAGTGTCTGGGAACACGCGCA | 1272 |
| Db | 1201 | GCCCCAGCGTACTTGGCAATGCGGGCCCTGTTTCTGGAGTGTCTGGGAACACGCGCA | 1260 |
| QY | 1273 | GTGCCCCGTACGGGTGTCTCTAAGACGCACTGCCCGCTCGGAGCTCGGTCACCCAGC | 1332 |
| Db | 1261 | GTGCCCCGTACGGGTGTCTCTAAGACGCACTGCCCGCTCGGAGCTCGGTCACCCAGC | 1320 |
| QY | 1333 | AGCGGTGTCTGTCCCGGGGAGAGCCCCAGGGCTCTGTGGGGCCCCCGGAGGAGGA | 1392 |

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| Db | 1321 | AGCCGGTGTCTGTCCCGGGAGAACCCAGGGTCTGTGGCGCCCCCGAGGAGGAGA | 1380 |
| QY | 1393 | CACAGACCCCGCTGCGCTGTGTCAGCTGCTCCGCGACACACAGCAGCCCTGGCAGGTGTA | 1452 |
| Db | 1381 | CACAGACCCCGCTGCGCTGTGTCAGCTGCTCCGCGACACACAGCAGCCCTGGCAGGTGTA | 1440 |
| QY | 1453 | CGGCTTGTGGGGCGCTGCCTGCGCGCGCTGGTGGTCCCCAGCCCTCTGGGCTCCAGGCA | 1512 |
| Db | 1441 | CGGCTTGTGGGGCGCTGCCTGCGCGCGCTGGTGGTCCCCAGCCCTCTGGGCTCCAGGCA | 1500 |
| QY | 1513 | CAACGAACCGCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA | 1572 |
| Db | 1501 | CAACGAACCGCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA | 1560 |
| QY | 1573 | GCTCTCGCTGAGGAGCTGACGTGGAAGATCAGCGTGGGACTGCGCTTGGCTGCGCAG | 1632 |
| Db | 1561 | GCTCTCGCTGAGGAGCTGACGTGGAAGATCAGCGTGGGACTGCGCTTGGCTGCGCAG | 1620 |
| QY | 1633 | GAGCCAGGGGTGGCTGTGTTCCGGCGCAGACACCGTCTGCGTGAGGAGATCTCTGGC | 1692 |
| Db | 1621 | GAGCCAGGGGTGGCTGTGTTCCGGCGCAGACACCGTCTGCGTGAGGAGATCTCTGGC | 1680 |
| QY | 1693 | CAAGTCTCTGACCTGGCTGATGACTGTCTACGTCTGAGCTGCTCAGGTCTTCTTTTA | 1752 |
| Db | 1681 | CAAGTCTCTGACCTGGCTGATGACTGTCTACGTCTGAGCTGCTCAGGTCTTCTTTTA | 1740 |
| QY | 1753 | TGTCACGAGACACAGCTTTTCAAAAGAACAGAGCTCTTTTTCACCGGAAGAGTGTGGAG | 1812 |
| Db | 1741 | TGTCACGAGACACAGCTTTTCAAAAGAACAGAGCTCTTTTTCACCGGAAGAGTGTGGAG | 1800 |
| QY | 1813 | CAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC | 1872 |
| Db | 1801 | CAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC | 1860 |
| QY | 1873 | GGAGCAGAGTTCAGGACGATCGGGAGCCAGGCCCGCTGCTGAGCTCCAGACTCCG | 1932 |
| Db | 1861 | GGAGCAGAGTTCAGGACGATCGGGAGCCAGGCCCGCTGCTGAGCTCCAGACTCCG | 1920 |
| QY | 1933 | CTTTCATCCCCAAGCTGACGGCTGCGGCCCATTTGTGAACATGACTACGTCTGGGAGC | 1992 |
| Db | 1921 | CTTTCATCCCCAAGCTGACGGCTGCGGCCCATTTGTGAACATGACTACGTCTGGGAGC | 1980 |
| QY | 1993 | CAGAACGTTCGCGAGAGAAAGAGGGCGGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT | 2052 |
| Db | 1981 | CAGAACGTTCGCGAGAGAAAGAGGGCGGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT | 2040 |
| QY | 2053 | CAGCGTCTCAACTACGAGCGGCGCGCGCCCGCTCTGCGCGCTCTGTGCTGGG | 2112 |
| Db | 2041 | CAGCGTCTCAACTACGAGCGGCGCGCGCCCGCTCTGCGCGCTCTGTGCTGGG | 2100 |
| QY | 2113 | CCTGGACGATATCCACAGGGCTTGGCGCACCTTCTGCTGCTGTGGGGGCCAGGAGCC | 2172 |
| Db | 2101 | CCTGGACGATATCCACAGGGCTTGGCGCACCTTCTGCTGCTGTGGGGGCCAGGAGCC | 2160 |
| QY | 2173 | GCCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGGTACGACACCATCCCCA | 2232 |
| Db | 2161 | GCCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGGTACGACACCATCCCCA | 2220 |
| QY | 2233 | GGACAGCTCAGGAGTTCATCGCCAGCATCATCAAAACCCAGAACACGTAAGTGGTGG | 2292 |
| Db | 2221 | GGACAGCTCAGGAGTTCATCGCCAGCATCATCAAAACCCAGAACACGTAAGTGGTGG | 2280 |
| QY | 2293 | TCGGTATGCGCTGCTCAGAAAGCGGCCATTTGGCACGTCGCGAAGGCTTTCAAGAGCA | 2352 |
| Db | 2281 | TCGGTATGCGCTGCTCAGAAAGCGGCCATTTGGCACGTCGCGAAGGCTTTCAAGAGCA | 2340 |
| QY | 2353 | CGTCTCTACCTGTACAGACCTTCCAGCCGTACATCGCAGTTCGTGGCTACCTGCAAGGA | 2412 |
| Db | 2341 | CGTCTCTACCTGTACAGACCTTCCAGCCGTACATCGCAGTTCGTGGCTACCTGCAAGGA | 2400 |
| QY | 2413 | GACACGCGCTGAGGGATGCGGTGCTCATCGACGAGCTCTCTCTCTGAATGAGGCCAG | 2472 |

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-Sep-2001
APPLICATION NUMBER: US/09/953,052
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
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REFERENCE/DOCKET NUMBER: 015389-00360005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:

NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse transcriptase (hTRT)"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
us-09-953-052-1

Query Match 99.6%; Score 3784.4; DB 10; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 73 GCGCGTCCCGCTGCGGAGCCGTGGCGCTCCCTGCTGCGCAGCAGCACTACCGCGAGGTGCT 132
DB 61 GCGCGTCCCGCTGCGGAGCCGTGGCGCTCCCTGCTGCGCAGCAGCACTACCGCGAGGTGCT 120
QY 133 GCGCGTGGCACGTGCTGGGGCGCTGGGGCCCGCAGGGCTGGGGGTGGTGGACGCCGG 192

DB 121 GCGCGTGGCACGTTCTGTTGGGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTCAGCGCGG 180
QY 193 GGACCCGGGGCTTTCCGGCGCTGGTGGCCCCAGTGCCTGGTGGTGGTGGTGGTGGTGGTGG 252
DB 181 GGACCCGGGGCTTTCCGGCGCTGGTGGCCCCAGTGCCTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 253 AGGGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGGTGCTTCCTGCTGAAGAGTGTGTGGC 312
DB 241 AGGGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGGTGCTTCCTGCTGAAGAGTGTGTGGC 300
QY 313 CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGGGAAGACGCTGCTGCGCTTCGCGCTTCGC 372
DB 301 CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGGGAAGACGCTGCTGCGCTTCGCGCTTCGC 360
QY 373 GCTGCTGGACGGGGCGCGGGGGCCCCCGCGAGGCTTTCACACACAGCGTGGCGAGCTA 432
DB 361 GCTGCTGGACGGGGCGCGGGGGCCCCCGCGAGGCTTTCACACACAGCGTGGCGAGCTA 420
QY 433 CCGTGGCCACACAGGTGACCGACGCTGCTGGGGGGAGGGGGCGTGGGGGGTGTGCTGGC 492
DB 421 CCGTGGCCACACAGGTGACCGACGCTGCTGGGGGGAGGGGGCGTGGGGGGTGTGCTGGC 480
QY 493 CCGCGTGGGGACGACGCTGCTGCTTCACTTGGCAGCGCTGCGCGCTCTTTCTGCTGGT 552
DB 481 CCGCGTGGGGACGACGCTGCTGCTTCACTTGGCAGCGCTGCGCGCTCTTTCTGCTGGT 540
QY 553 GGTCTCCAGCTGCGCTTACCAGTGTGCGGGCGCGCGCTGTACAGTCTGGCGCTGCCAC 612
DB 541 GGTCTCCAGCTGCGCTTACCAGTGTGCGGGCGCGCGCTGTACAGTCTGGCGCTGCCAC 600
QY 613 TCAGGCGCGCGCGCGCGCGCGCTAGTGGACCCCGAAGCGCTGTGGATGCGAAGCGGC 672
DB 601 TCAGGCGCGCGCGCGCGCGCGCTAGTGGACCCCGAAGCGCTGTGGATGCGAAGCGGC 660
QY 673 CTGGAACCATAGCGTCAGGGAGCGCGGGTCCCGCTGGGCTGTCAGCGCCCGGCTGGAG 732
DB 661 CTGGAACCATAGCGTCAGGGAGCGCGGGTCCCGCTGGGCTGTCAGCGCCCGGCTGGAG 720
QY 733 GAGGCGGGGGCAGTCCACGCGCAAGTGTGCGCTTTCGCCAAGAGGCCCGAGGGCTGGCGC 792
DB 721 GAGGCGGGGGCAGTCCACGCGCAAGTGTGCGCTTTCGCCAAGAGGCCCGAGGGCTGGCGC 780
QY 793 TGCCCTTGAGCCGAGGGAGCGCGCTTGGGCGAGGGTCTTGGGCCACCCCGGGCAGGAC 852
DB 781 TGCCCTTGAGCCGAGGGAGCGCGCTTGGGCGAGGGTCTTGGGCCACCCCGGGCAGGAC 840
QY 853 GCGTGGACCGAGTGACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
DB 841 GCGTGGACCGAGTGACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 913 CACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTCCACCCATCCCGTGGGGCGGCCA 972
DB 901 CACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTCCACCCATCCCGTGGGGCGGCCA 960
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QY 1093 GCCTCTCTTCTACTAGCTCTCTGAGGGCGCGAGCTGACCTGAGCTCGGAGGCTCGGGA 1152
DB 1081 GCCTCTCTTCTACTAGCTCTCTGAGGGCGCGAGCTGACCTGAGGCTCGGAGGCTCGGGA 1140
QY 1153 GACCATCTTCTTGGGTTCAGGCGCTTGGATGCCAGGAGTCCCGCGAGGTGGCCCGCT 1212
DB 1141 GACCATCTTCTTGGGTTCAGGCGCTTGGATGCCAGGAGTCCCGCGAGGTGGCCCGCT 1200
QY 1213 GCGCCAGCGCTACTGGCAATGCGGGCGCTTCTTCTGAGAGTGTGTTGGGAACACGCGCA 1272
DB 1201 GCGCCAGCGCTACTGGCAATGCGGGCGCTTCTTCTGAGAGTGTGTTGGGAACACGCGCA 1260

| | | | |
|----|------|---|------|
| QY | 1273 | GTGCCCCACGGGTGCTCCTCAAGACGACCTGCGCGCTGCGAGCTGCGGTCAACCCACG | 1332 |
| DB | 1261 | GTGCCCCACGGGTGCTCCTCAAGACGACCTGCGCGCTGCGAGCTGCGGTCAACCCACG | 1320 |
| QY | 1333 | AGCCGGTGTCTGTGCCCGGAGAACCCAGGGCTCTGTGGCGGCCCGCCGAGGAGGGA | 1392 |
| DB | 1321 | AGCCGGTGTCTGTGCCCGGAGAACCCAGGGCTCTGTGGCGGCCCGCCGAGGAGGGA | 1380 |
| QY | 1393 | CACAGACCCCGTGCCTGGTGGTACAGCTGCTGGCCGACACAGCAGCCCTGGCAGGTGA | 1452 |
| DB | 1381 | CACAGACCCCGTGCCTGGTGGTACAGCTGCTGGCCGACACAGCAGCCCTGGCAGGTGA | 1440 |
| QY | 1453 | CGGCTTCGTGGGGGCTGCCTGCGCGCGCTGGTGGCCCGCCAGGCCCTGCGGCTCCAGCA | 1512 |
| DB | 1441 | CGGCTTCGTGGGGGCTGCCTGCGCGCGCTGGTGGCCCGCCAGGCCCTGCGGCTCCAGCA | 1500 |
| QY | 1513 | CAACGAACCGCGCTTCCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA | 1572 |
| DB | 1501 | CAACGAACCGCGCTTCCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA | 1560 |
| QY | 1573 | GCTCTCGCTGACGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGGTGGCTGGCGAG | 1632 |
| DB | 1561 | GCTCTCGCTGACGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGGTGGCTGGCGAG | 1620 |
| QY | 1633 | GAGCCACGGGTGGCTGTGTTCCGGCGCGAGACACCGCTCTGCGTGAGGAGATCCTGCG | 1692 |
| DB | 1621 | GAGCCACGGGTGGCTGTGTTCCGGCGCGAGACACCGCTCTGCGTGAGGAGATCCTGCG | 1680 |
| QY | 1693 | CAAGTTCCTGCACTGGCTGATGAGTGTAGCTCGTCGAGTGTCTCAGGTCTTCTTTTA | 1752 |
| DB | 1681 | CAAGTTCCTGCACTGGCTGATGAGTGTAGCTCGTCGAGTGTCTCAGGTCTTCTTTTA | 1740 |
| QY | 1753 | TGTCAGGAGACCGTTCCTCAAGAACACAGGCTCTTTTTCACCGGAAGTGTCTGGAG | 1812 |
| DB | 1741 | TGTCAGGAGACCGTTCCTCAAGAACACAGGCTCTTTTTCACCGGAAGTGTCTGGAG | 1800 |
| QY | 1813 | CAAGTTGCAAGCATGGAATCAGACACACTTGAAGAGGTGACGCTGCGGGAGCTGTC | 1872 |
| DB | 1801 | CAAGTTGCAAGCATGGAATCAGACACACTTGAAGAGGTGACGCTGCGGGAGCTGTC | 1860 |
| QY | 1873 | GGAACAGAGTTCAGCAGCATCGGGAAGCAGGCCCGCTGCTGACGTCCAGACTCGG | 1932 |
| DB | 1861 | GGAACAGAGTTCAGCAGCATCGGGAAGCAGGCCCGCTGCTGACGTCCAGACTCGG | 1920 |
| QY | 1933 | CTTCATCCCAAGCTGACGGCTGCGGCCGATGTGAACATGGAATGACGTGCGGGAGC | 1992 |
| DB | 1921 | CTTCATCCCAAGCTGACGGCTGCGGCCGATGTGAACATGGAATGACGTGCGGGAGC | 1980 |
| QY | 1993 | CAGACGTTCCGACAGAAAGGCGGAGCGTCTACCTCGAGGGTGAAGGCACTGTT | 2052 |
| DB | 1981 | CAGAACGTTCCGACAGAAAGGCGGAGCGTCTACCTCGAGGGTGAAGGCACTGTT | 2040 |
| QY | 2053 | CAGCGTGTCAACTACGAGCGGGCGGCGGCCCGCTGCTGGCGCTCTGTGCTGGG | 2112 |
| DB | 2041 | CAGCGTGTCAACTACGAGCGGGCGGCGGCCCGCTGCTGGCGCTCTGTGCTGGG | 2100 |
| QY | 2113 | CCTGGACGATATCCACAGGGCTGGCGACCTTGTGTGCTGTGCGGGCCCGAGACCC | 2172 |
| DB | 2101 | CCTGGACGATATCCACAGGGCTGGCGACCTTGTGTGCTGTGCGGGCCCGAGACCC | 2160 |
| QY | 2173 | GCCGCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGGTACGACACATCCCCCA | 2232 |
| DB | 2161 | GCCGCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGGTACGACACATCCCCCA | 2220 |
| QY | 2233 | GGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGACACGTAAGTGGCG | 2292 |
| DB | 2221 | GGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGACACGTAAGTGGCG | 2280 |
| QY | 2293 | TCGGTATGCCGTGTCCAGAAAGGCGCCCATGGGCACGTCGCGAAGGCTTCAAGAGCA | 2352 |
| DB | 2281 | TCGGTATGCCGTGTCCAGAAAGGCGCCCATGGGCACGTCGCGAAGGCTTCAAGAGCA | 2340 |

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| QY | 2353 | CGTCTCTACTGTGACAGACCTCCAGCGGTACATCGACAGTTCTGGCTCACTCGAGA | 2412 |
| DB | 2341 | CGTCTCTACTGTGACAGACCTCCAGCGGTACATCGACAGTTCTGGCTCACTCGAGA | 2400 |
| QY | 2413 | GACCAACCCCGTGTAGGGATGCCGTGTCATCAGCAGAGCTCCTCCCTGAATGAGGCCAG | 2472 |
| DB | 2401 | GACCAACCCCGTGTAGGGATGCCGTGTCATCAGCAGAGCTCCTCCCTGAATGAGGCCAG | 2460 |
| QY | 2473 | CAGTGGCTCTTCGACAGCTTCTTCCATAGCTTCATGTGCCACACGCGTGCATCAGGGG | 2532 |
| DB | 2461 | CAGTGGCTCTTCGACAGCTTCTTCCATAGCTTCATGTGCCACACGCGTGCATCAGGGG | 2520 |
| QY | 2533 | CAAGTCTTAGCTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG | 2592 |
| DB | 2521 | CAAGTCTTAGCTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG | 2580 |
| QY | 2593 | CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGGGGGATTCGGCGGAGGGGCT | 2652 |
| DB | 2581 | CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGGGGGATTCGGCGGAGGGGCT | 2640 |
| QY | 2653 | GCTCTCGCTTGGTGGATGATTTCTTGTGTGACACCTCACCACCGCGAAAC | 2712 |
| DB | 2641 | GCTCTCGCTTGGTGGATGATTTCTTGTGTGACACCTCACCACCGCGAAAC | 2700 |
| QY | 2713 | CTTCTCTCAGGACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGAACCTTGGGAA | 2772 |
| DB | 2701 | CTTCTCTCAGGACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGAACCTTGGGAA | 2760 |
| QY | 2773 | GACAGTGTGAACCTTCCCTGTAGAAAGAGAGCCCTGGGTGCGACGGCTTTTTCAGAT | 2832 |
| DB | 2761 | GACAGTGTGAACCTTCCCTGTAGAAAGAGAGCCCTGGGTGCGACGGCTTTTTCAGAT | 2820 |
| QY | 2833 | GCCGCGCCACGGCTTATTCCTGCTGGCGGCTGCTGTGTGATACCCGACCCCTGGAGT | 2892 |
| DB | 2821 | GCCGCGCCACGGCTTATTCCTGCTGGCGGCTGCTGTGTGATACCCGACCCCTGGAGT | 2880 |
| QY | 2893 | GCAGAGGACACTCTCCAGTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACGG | 2952 |
| DB | 2881 | GCAGAGGACACTCTCCAGTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACGG | 2940 |
| QY | 2953 | CGGCTTCAAGGCTGGGAGAACATCGTTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG | 3012 |
| DB | 2941 | CGGCTTCAAGGCTGGGAGAACATCGTTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG | 3000 |
| QY | 3013 | TCACAGCTGTCTTGTGATTTGACGTTGAACAGCCTCCAGAGCGTGTGCACCAACATCTA | 3072 |
| DB | 3001 | TCACAGCTGTCTTGTGATTTGACGTTGAACAGCCTCCAGAGCGTGTGCACCAACATCTA | 3060 |
| QY | 3073 | CAAGATCTCTGCTGCGAGCGGTACAGTTTTCACGATGTGTGTGAGCTCCCATTTCA | 3132 |
| DB | 3061 | CAAGATCTCTGCTGCGAGCGGTACAGTTTTCACGATGTGTGTGAGCTCCCATTTCA | 3120 |
| QY | 3133 | TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGCGTCTCTGACACGGCTCCCT | 3192 |
| DB | 3121 | TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGCGTCTCTGACACGGCTCCCT | 3180 |
| QY | 3193 | CTGCTACTCTTCCATTCCTGAAGCAAGACGAGGATGTGCTGGGGGCAAGGGCGCGC | 3252 |
| DB | 3181 | CTGCTACTCTTCCATTCCTGAAGCAAGACGAGGATGTGCTGGGGGCAAGGGCGCGC | 3240 |
| QY | 3253 | CGGCGCTCTGCGCTCCGAGCGGTGAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT | 3312 |
| DB | 3241 | CGGCGCTCTGCGCTCCGAGCGGTGAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT | 3300 |
| QY | 3313 | GACTCGACACGCTGCTCAGTCTAGTGGCTGCTGCGGCTGCTGAGGCGGACGCGCA | 3372 |
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| QY | 3373 | GCTGAGTCGGAGCTTCCCGGGGACGCTGACTGCTGAGGCGGACGCGCAACCCGCG | 3432 |
| DB | 3361 | GCTGAGTCGGAGCTTCCCGGGGACGCTGACTGCTGAGGCGGACGCGCAACCCGCG | 3420 |
| QY | 3433 | ACTGCCCTCAGACTTCAAGACCATCTGAGTGTGCGACCCGCGCCACAGCCAGCGCGA | 3492 |

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Db 3601 CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCCTGAGGCCCTGAGGCCCTGAGGCCCTG 3660
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Db 3781 CCAGAT 3786

RESULT 5

US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
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; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US

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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "htrt"
/note= "human telomerase reverse
transcriptase (htrt) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
Query Match 99.6%; Score 3784.4; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 GCAGCGCTGCTGCTGCGACAGTGGGAAGCCCTGGCCCCCGGCCACACCCCGCATGCC 72
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QY 73 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 132
Db 61 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
QY 133 GCGCGTGGCCACAGTTCGTGCGGGCCCTGGGGCCCCCAGGGCTGGCGGTGTGTGAGCGCGG 192
Db 121 GCGCGTGGCCACAGTTCGTGCGGGCCCTGGGGCCCCCAGGGCTGGCGGTGTGTGAGCGCGG 180
QY 193 GGACCGCGGGGCTTTCCGGCGGCTGGTGGGCCAGTGGCTGGTGGTGGTGGTGGTGGTGG 252
Db 181 GGACCGCGGGGCTTTCCGGCGGCTGGTGGGCCAGTGGCTGGTGGTGGTGGTGGTGGTGG 240
QY 253 ACGGCGCGCCCGCGCGCCCTTCCCTCCCGCAGGTGCTGCTGAGGAGTGGTGGTGGTGG 312
Db 241 ACGGCGCGCCCGCGCGCCCTTCCCTCCCGCAGGTGCTGCTGAGGAGTGGTGGTGGTGG 300
QY 313 CCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTTCGC 372
Db 301 CCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTTCGC 360
QY 373 GCTGCTGGAGGGGGCGCGGG 432
Db 361 GCTGCTGGAGGG 420
QY 433 CTTGCCCAACACAGCTGACCGACACACTGCGGGGGAGGGGGGGGGGGGGGGGGGGGGGG 492
Db 421 CTTGCCCAACACAGCTGACCGACACACTGCGGGGGAGGGGGGGGGGGGGGGGGGGGGGG 480
QY 493 CCGCGTGGCGGACGAGTGTGCTTCACTTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 552
Db 481 CCGCGTGGCGGACGAGTGTGCTTCACTTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 540
QY 553 GGCTCCCGAGGTGCGCTTACCAAGTGTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 612
Db 541 GGCTCCCGAGGTGCGCTTACCAAGTGTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 600
QY 613 TCAGGGCCGG 672
Db 601 TCAGGGCCGG 660
QY 673 CTGGAACCATAGCGTTCAGGGAGGCGGGGTTCCTGGGGCTTCCTGGGGCTTCCTGGGGCT 732
Db 661 CTGGAACCATAGCGTTCAGGGAGGCGGGGTTCCTGGGGCTTCCTGGGGCTTCCTGGGGCT 720
QY 733 GAGGCGGGGGGGGAGTGGCCAGCCGGAAGTCTGCCGTTCGCCCAAGAGGGCCAGGGCGT 792

| | | | |
|----|------|--|------|
| Db | 721 | GAGGCGGGGGCAGTGCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGCGTGGCGC | 780 |
| QY | 793 | TGCCCCGTAGCCGGAGCGACGCCGTTGGGACAGGGTCTTGGGCCACCCCGGGCAGGAC | 852 |
| Db | 781 | TGCCCCGTAGCCGGAGCGACGCCGTTGGGACAGGGTCTTGGGCCACCCCGGGCAGGAC | 840 |
| QY | 853 | GGGTGACCGAGTACCGGTGGTCTCTGTGTGTGTCACTGCGCAGACCGCGCGAAGAAGC | 912 |
| Db | 841 | GGGTGACCGAGTACCGGTGGTCTCTGTGTGTGTCACTGCGCAGACCGCGCGAAGAAGC | 900 |
| QY | 913 | CACCTCTTTGGAGGTGGGCTCTGTGGACGCGCACCTGCCACCTCCACCCATCCGTTGGGCGGCA | 972 |
| Db | 901 | CACCTCTTTGGAGGTGGGCTCTGTGGACGCGCACCTGCCACCTCCACCCATCCGTTGGGCGGCA | 960 |
| QY | 973 | GCACACGGGGCGCCCCCATCCACATCGGGGCCACACGTCTCCTGGGACACGCTTGTC | 1032 |
| Db | 961 | GCACACGGGGCGCCCCCATCCACATCGGGGCCACACGTCTCCTGGGACACGCTTGTC | 1020 |
| QY | 1033 | CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCTCAGCGCACAGGAGCAGCTGG | 1092 |
| Db | 1021 | CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCTCAGCGCACAGGAGCAGCTGG | 1080 |
| QY | 1093 | GCCCTCTCTTACTCAGCTCTCTGAGGCCACGCTGACTGGCGTTCGGAGGCTCGTGG | 1152 |
| Db | 1081 | GCCCTCTCTTACTCAGCTCTCTGAGGCCACGCTGACTGGCGTTCGGAGGCTCGTGG | 1140 |
| QY | 1153 | GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCGCT | 1212 |
| Db | 1141 | GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCGCT | 1200 |
| QY | 1213 | GCCCCAGCGCTACTTGGCAAAATCGGCCCTGTCTTCTGGAGCTGTGGGAACACGCGCA | 1272 |
| Db | 1201 | GCCCCAGCGCTACTTGGCAAAATCGGCCCTGTCTTCTGGAGCTGTGGGAACACGCGCA | 1260 |
| QY | 1273 | GTGCCCTTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGGTCAACCCAGC | 1332 |
| Db | 1261 | GTGCCCTTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGGTCAACCCAGC | 1320 |
| QY | 1333 | AGCCGGTGTCTGTGCCGGGAGAACCCAGGGCTGTGTGGGGCCCCCGAGGAGGAGGA | 1392 |
| Db | 1321 | AGCCGGTGTCTGTGCCGGGAGAACCCAGGGCTGTGTGGGGCCCCCGAGGAGGAGGA | 1380 |
| QY | 1393 | CACAGACCCCGCTGCCTGGTGCAGTGTCTCCGCCAGACACAGCAGCCCTGGCAGGTGA | 1452 |
| Db | 1381 | CACAGACCCCGCTGCCTGGTGCAGTGTCTCCGCCAGACACAGCAGCCCTGGCAGGTGA | 1440 |
| QY | 1453 | CGGCTTCTGCGGGCTGCCTGCGCGGCTGTGTGCCAGCCCTGCGGGTCCAGGCA | 1512 |
| Db | 1441 | CGGCTTCTGCGGGCTGCCTGCGCGGCTGTGTGCCAGCCCTGCGGGTCCAGGCA | 1500 |
| QY | 1513 | CAACGAACCCCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAACATGCCAA | 1572 |
| Db | 1501 | CAACGAACCCCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAACATGCCAA | 1560 |
| QY | 1573 | GCTCTCGGTGACGAGCTGACGTGAGATGAGCGTGGGGACTGGGCTGGCTGGCGAG | 1632 |
| Db | 1561 | GCTCTCGGTGACGAGCTGACGTGAGATGAGCGTGGGGACTGGGCTGGCTGGCGAG | 1620 |
| QY | 1633 | GAGCCACAGGGTGGCTGTGTTCGGCGCGCAGACACCGCTCTGCGTGGAGAGATCCTGGC | 1692 |
| Db | 1621 | GAGCCACAGGGTGGCTGTGTTCGGCGCGCAGACACCGCTCTGCGTGGAGAGATCCTGGC | 1680 |
| QY | 1693 | CAAGTCTCTGCACTGGCTGATGAGTGTGTACGTCTGCGAGCTGCTCAGGTCTTTCTTTA | 1752 |
| Db | 1681 | CAAGTCTCTGCACTGGCTGATGAGTGTGTACGTCTGCGAGCTGCTCAGGTCTTTCTTTA | 1740 |
| QY | 1753 | TGTCAGGAGACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCTGGAG | 1812 |
| Db | 1741 | TGTCAGGAGACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCTGGAG | 1800 |
| QY | 1813 | CAAGTTGAAAGCATTTGGAATCAGACACGACTTGAAGGGGTGCAGCTCGGGAGCTGTC | 1872 |
| Db | 1801 | CAAGTTGAAAGCATTTGGAATCAGACACGACTTGAAGGGGTGCAGCTCGGGAGCTGTC | 1860 |
| QY | 1873 | GGAAAGCAGAGGTACGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGCTCAGACTCCG | 1932 |
| Db | 1861 | GGAAAGCAGAGGTACGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGCTCAGACTCCG | 1920 |
| QY | 1933 | CTTTCATCCCAAGACCTGACGGCTGCGGCCGATTGTGAACATGGACTAGCTGCTGGGAGC | 1992 |
| Db | 1921 | CTTTCATCCCAAGACCTGACGGCTGCGGCCGATTGTGAACATGGACTAGCTGCTGGGAGC | 1980 |
| QY | 1993 | CAGACGTTTCCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT | 2052 |
| Db | 1981 | CAGACGTTTCCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT | 2040 |
| QY | 2053 | CAGCGTGTCAACTACGAGCGGGCGCGGCCCGCCCTCTGTTGGGCGCTCTGTTGCTGG | 2112 |
| Db | 2041 | CAGCGTGTCAACTACGAGCGGGCGCGGCCCGCCCTCTGTTGGGCGCTCTGTTGCTGG | 2100 |
| QY | 2113 | CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCACAGACCC | 2172 |
| Db | 2101 | CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCACAGACCC | 2160 |
| QY | 2173 | GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCATCCCCCA | 2232 |
| Db | 2161 | GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCATCCCCCA | 2220 |
| QY | 2233 | GGACAGGCTACGGAGGTTCATGCCAGCATCATCAAAACCCAGAACACGCTACTGCTGGC | 2292 |
| Db | 2221 | GGACAGGCTACGGAGGTTCATGCCAGCATCATCAAAACCCAGAACACGCTACTGCTGGC | 2280 |
| QY | 2293 | TGCGTATGCCGTGGTCCAGAAAGCCCATGGGACGCTCCGCAAGGCTTCAAGAGCCA | 2352 |
| Db | 2281 | TGCGTATGCCGTGGTCCAGAAAGCCCATGGGACGCTCCGCAAGGCTTCAAGAGCCA | 2340 |
| QY | 2353 | CGTCTCTACTTTGACAGACCTCCAGCCGTACATCGACAGCTTCGTGGCTCACCCTGACGA | 2412 |
| Db | 2341 | CGTCTCTACTTTGACAGACCTCCAGCCGTACATCGACAGCTTCGTGGCTCACCCTGACGA | 2400 |
| QY | 2413 | GACCAGCCGCTGAGGGATGCCGTGTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG | 2472 |
| Db | 2401 | GACCAGCCGCTGAGGGATGCCGTGTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG | 2460 |
| QY | 2473 | CAGTGGCTCTTCGACGCTTCTCCTACGCTTCATGTGCCACACGCGCTGCGCATAGGGG | 2532 |
| Db | 2461 | CAGTGGCTCTTCGACGCTTCTCCTACGCTTCATGTGCCACACGCGCTGCGCATAGGGG | 2520 |
| QY | 2533 | CAAGTCTACGCTTCAGTGGCGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG | 2592 |
| Db | 2521 | CAAGTCTACGCTTCAGTGGCGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG | 2580 |
| QY | 2593 | CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGGGGGATTCGGGGGACCGGCT | 2652 |
| Db | 2581 | CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGGGGGATTCGGGGGACCGGCT | 2640 |
| QY | 2653 | GCTCTGCTGCTTGGTGGATGATTCTTGTGTGTGACACCTCACCCTCACCACCGCAAAAC | 2712 |
| Db | 2641 | GCTCTGCTGCTTGGTGGATGATTCTTGTGTGTGACACCTCACCCTCACCACCGCAAAAC | 2700 |
| QY | 2713 | CTTCTCTCAGACCCCTGGTCCGAGGTCCTCCTGAGTATGCTGCTGCTGAACCTTCGGGAA | 2772 |
| Db | 2701 | CTTCTCTCAGACCCCTGGTCCGAGGTCCTCCTGAGTATGCTGCTGCTGAACCTTCGGGAA | 2760 |
| QY | 2773 | GACAGTGTGAACTTCCCTGTAGAAGACAGGCCCCCTGGGTGGCACGGCTTTTGTTCAGAT | 2832 |
| Db | 2761 | GACAGTGTGAACTTCCCTGTAGAAGACAGGCCCCCTGGGTGGCACGGCTTTTGTTCAGAT | 2820 |
| QY | 2833 | GCCGGCCACGGCCTATTCCTCTGGTGGCGCTGCTGCTGGATACCCGACCCCTGGAGGT | 2892 |
| Db | 2821 | GCCGGCCACGGCCTATTCCTCTGGTGGCGCTGCTGCTGGATACCCGACCCCTGGAGGT | 2880 |
| QY | 2893 | GCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCGAGTCTCACCTTCAACCG | 2952 |
| Db | 2881 | GCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCGAGTCTCACCTTCAACCG | 2940 |

| | | | |
|----|------|---|------|
| Qy | 2953 | CGGCTTCAAGGCTGGGAGAACATGCGTCGAAACTCTTTGGGCTCTTGGGCTGGAAGTG | 3012 |
| Db | 2941 | CGGCTTCAAGGCTGGGAGAACATGCGTCGAAACTCTTTGGGCTCTTGGGCTGGAAGTG | 3000 |
| Qy | 3013 | TCACAGCCTGTTCCTGATTTGCAAGTGAAACAGCCTCCACAGCGTGTGCACCAACATCTA | 3072 |
| Db | 3001 | TCACAGCCTGTTCCTGATTTGCAAGTGAAACAGCCTCCACAGCGTGTGCACCAACATCTA | 3060 |
| Qy | 3073 | CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCAATGTGTGCTGCAGCTCCCATTTCA | 3132 |
| Db | 3061 | CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCAATGTGTGCTGCAGCTCCCATTTCA | 3120 |
| Qy | 3133 | TCAGCAAGTTTGGAAAGACCCACATTTTTCCTTCGCGGTATCTCTGCACAGGCGTCCCT | 3192 |
| Db | 3121 | TCAGCAAGTTTGGAAAGACCCACATTTTTCCTTCGCGGTATCTCTGCACAGGCGTCCCT | 3180 |
| Qy | 3193 | CTGCTACTCCTCCTGAAAGCAACGACGAGGATGTCTGCTGGGGCCAAAGGCGCGCG | 3252 |
| Db | 3181 | CTGCTACTCCTCCTGAAAGCAACGACGAGGATGTCTGCTGGGGCCAAAGGCGCGCG | 3240 |
| Qy | 3253 | CGGCGCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTAAGCT | 3312 |
| Db | 3241 | CGGCGCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTAAGCT | 3300 |
| Qy | 3313 | GACTCGACACCGTGTCACTTACCTACGTCGCACATCTCTGGGTCACTCAGGACACCCAGAGCA | 3372 |
| Db | 3301 | GACTCGACACCGTGTCACTTACGTCGCACATCTCTGGGTCACTCAGGACACCCAGAGCA | 3360 |
| Qy | 3373 | GCTGAGTCGAAAGTCCCGGGGACGAGCTGACTGCCCTGGAGCGCCAGCCAAACCGCGC | 3432 |
| Db | 3361 | GCTGAGTCGAAAGTCCCGGGGACGAGCTGACTGCCCTGGAGCGCCAGCCAAACCGCGC | 3420 |
| Qy | 3433 | ACTGCCCTCAGACTTCAAGACCATCTCGGACTGATGGCCACCGCCCGCCAGCCAGCCCGA | 3492 |
| Db | 3421 | ACTGCCCTCAGACTTCAAGACCATCTCGGACTGATGGCCACCGCCCGCCAGCCAGCCCGA | 3480 |
| Qy | 3493 | GAGCAGACACCAAGCAGCCCTGTACGCGCGGGCTCTACGTCCCAGGAGGAGGGGGGGCC | 3552 |
| Db | 3481 | GAGCAGACACCAAGCAGCCCTGTACGCGCGGGCTCTACGTCCCAGGAGGAGGGGGGGCC | 3540 |
| Qy | 3553 | CACACCCAGCGCCGACCCGCTGGAGTCTCAGGCGCTGAGTGAGTGTGGCCAGAGGCGTG | 3612 |
| Db | 3541 | CACACCCAGCGCCGACCCGCTGGAGTCTCAGGCGCTGAGTGAGTGTGGCCAGAGGCGTG | 3600 |
| Qy | 3613 | CATGTCGGCTGAAGGTGAGTGTCCGGCTGAGCGCTGAGCGAGTGTCACAGGCAAGGGCT | 3672 |
| Db | 3601 | CATGTCGGCTGAAGGTGAGTGTCCGGCTGAGCGCTGAGCGAGTGTCACAGGCAAGGGCT | 3660 |
| Qy | 3673 | GAGTGTCCAGCACACTGCGGCTTCTACTTCCCAAGGCTGGCGGTGCGCTCCACCCCA | 3732 |
| Db | 3661 | GAGTGTCCAGCACACTGCGGCTTCTACTTCCCAAGGCTGGCGGTGCGCTCCACCCCA | 3720 |
| Qy | 3733 | GGGCCAGCTTTTCTTACCAGGAGCGGGCTTCCACTCCCAATAGGAATAGTCCATCC | 3792 |
| Db | 3721 | GGGCCAGCTTTTCTTACCAGGAGCGGGCTTCCACTCCCAATAGGAATAGTCCATCC | 3780 |
| Qy | 3793 | CCTGAT | 3798 |
| Db | 3781 | CCAGAT | 3786 |

RESULT 7

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US-101-054-295-224
; Sequence 224, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
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; Harley, Calvin
; Andrews, William H.

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| | | | |
|----|------|---|------|
| Db | 241 | ACGGCCGCCCGCGCCGCCCTTCCTTCGGCAGGTGTCTCGCTGAAGGAGCTGGTGCG | 300 |
| QY | 313 | CCGAGTGTCTGCAGAGGCTGTGGAGCGCGGCGGAAGAACGTGCTGGCCCTTGGGCTTCGC | 372 |
| Db | 301 | CCGAGTGTCTGCAGAGGCTGTGGAGCGCGGCGGAAGAACGTGCTGGCCCTTGGGCTTCGC | 360 |
| QY | 373 | GCTGCTGGACGGGGCCCGGGGGCCCCCGAGGGCTTCACACCAGAGCTGCGCAGCTA | 432 |
| Db | 361 | GCTGCTGGACGGGGCCCGGGGGCCCCCGAGGGCTTCACACCAGAGCTGCGCAGCTA | 420 |
| QY | 433 | CTTGCCCAACACGGGTGACCGACACTGCGGGGGAGCGGGGGCTGCTGCTGCG | 492 |
| Db | 421 | CTTGCCCAACACGGGTGACCGACACTGCGGGGGAGCGGGGGCTGCTGCTGCG | 480 |
| QY | 493 | CGCGTGGGCGAGGAGTGTGTTACCTGCTGGCACGCTGGCGCTTTTGTGTGTGT | 552 |
| Db | 481 | CGCGTGGGCGAGGAGTGTGTTACCTGCTGGCACGCTGGCGCTTTTGTGTGTGT | 540 |
| QY | 553 | GGCTCCAGCTGCGCTACAGGTGTGCGGGCGCGCGTGTACAGCTCGGCGCTGCCAC | 612 |
| Db | 541 | GGCTCCAGCTGCGCTACAGGTGTGCGGGCGCGCGTGTACAGCTCGGCGCTGCCAC | 600 |
| QY | 613 | TCAGGCCCGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAACGGCG | 672 |
| Db | 601 | TCAGGCCCGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAACGGCG | 660 |
| QY | 673 | CTGGAAACATAGGTCAGGAGGCGCGGGTCCCGCTGGGCTGCGACGCCCGGGTGGAG | 732 |
| Db | 661 | CTGGAAACATAGGTCAGGAGGCGCGGGTCCCGCTGGGCTGCGACGCCCGGGTGGAG | 720 |
| QY | 733 | GAGCGCGGGGCGAGTGCACGCGAAGTCTGCGCTTGCCCAAGAGGCCCGAGGCGTGGCGC | 792 |
| Db | 721 | GAGCGCGGGGCGAGTGCACGCGAAGTCTGCGCTTGCCCAAGAGGCCCGAGGCGTGGCGC | 780 |
| QY | 793 | TGCCCCTAGCGCGGAGCGACGCCGCTTGGGACAGGGGTCTGGGCCCCACCCCGGGCAGGAC | 852 |
| Db | 781 | TGCCCCTAGCGCGGAGCGACGCCGCTTGGGACAGGGGTCTGGGCCCCACCCCGGGCAGGAC | 840 |
| QY | 853 | GGGTGACCGAGTGACCGTGTCTGCTGTGTGTGTACCTGCGCAGACCGCGCCGGAAGAC | 912 |
| Db | 841 | GGGTGACCGAGTGACCGTGTCTGCTGTGTGTGTACCTGCGCAGACCGCGCCGGAAGAC | 900 |
| QY | 913 | CACCTCTTTGGAGGTGCGCTCTCTGGCACGGGCCACTCCCACTCCGTTGGCGGCCCA | 972 |
| Db | 901 | CACCTCTTTGGAGGTGCGCTCTCTGGCACGGGCCACTCCCACTCCGTTGGCGGCCCA | 960 |
| QY | 973 | GCACACGGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTCC | 1032 |
| Db | 961 | GCACACGGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTCC | 1020 |
| QY | 1033 | CCGGTGTACCGGAGACCAAGCACTTCTCTACTCTCAGGGGCAAGGAGGAGTGGG | 1092 |
| Db | 1021 | CCGGTGTACCGGAGACCAAGCACTTCTCTACTCTCAGGGGCAAGGAGGAGTGGG | 1080 |
| QY | 1093 | GCCCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTCGTGA | 1152 |
| Db | 1081 | GCCCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTCGTGA | 1140 |
| QY | 1153 | GACCACTTCTTGGGTTCCAGGCCCTTGGATGCCAGGACTCCCGCAGGTTGCCCGGCT | 1212 |
| Db | 1141 | GACCACTTCTTGGGTTCCAGGCCCTTGGATGCCAGGACTCCCGCAGGTTGCCCGGCT | 1200 |
| QY | 1213 | GCCCCAGCGCTACTGCGCAATGGGCCCCCTGTTCTGGAGCTGCTTGGGAACCAACGCGCA | 1272 |
| Db | 1201 | GCCCCAGCGCTACTGCGCAATGGGCCCCCTGTTCTGGAGCTGCTTGGGAACCAACGCGCA | 1260 |
| QY | 1273 | GTGCCCTTACGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCACG | 1332 |
| Db | 1261 | GTGCCCTTACGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCACG | 1320 |
| QY | 1333 | AGCCGGTGTCTGTGCCCGGAGAACCCCGAGGGCTGTGTGGCGGCCCGCCGAGGAGGGA | 1392 |
| Db | 1321 | AGCCGGTGTCTGTGCCCGGAGAACCCCGAGGGCTGTGTGGCGGCCCGCCGAGGAGGGA | 1380 |
| QY | 1393 | CACAGACCCCGCTCGCCTGGTGCAGCTGCTCCGCCACACAGACAGACCCCTGGCAGTGA | 1452 |
| Db | 1381 | CACAGACCCCGCTCGCCTGGTGCAGCTGCTCCGCCACACAGACAGACCCCTGGCAGTGA | 1440 |
| QY | 1453 | CGGCTTCGTGCGGGCTGCTGCGCGGCTGTGTGCGCCACAGGCTCTGGGGCTCCAGGCA | 1512 |
| Db | 1441 | CGGCTTCGTGCGGGCTGCTGCGCGGCTGTGTGCGCCACAGGCTCTGGGGCTCCAGGCA | 1500 |
| QY | 1513 | CAACGAACCGCGCTTCTCAGGAACACCAAGAAAGTTTCATCTCCCTGGGAAGCATGCCAA | 1572 |
| Db | 1501 | CAACGAACCGCGCTTCTCAGGAACACCAAGAAAGTTTCATCTCCCTGGGAAGCATGCCAA | 1560 |
| QY | 1573 | GCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGCTGCGGACTGCGCTTGGCTGCGCAG | 1632 |
| Db | 1561 | GCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGCTGCGGACTGCGCTTGGCTGCGCAG | 1620 |
| QY | 1633 | GAGCCAGGGGTTGGGCTGTTCGGCGCCAGACACCGCTCTCGCTGAGGAGATCTCTGGC | 1692 |
| Db | 1621 | GAGCCAGGGGTTGGGCTGTTCGGCGCCAGACACCGCTCTCGCTGAGGAGATCTCTGGC | 1680 |
| QY | 1693 | CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGCGAGCTGCTCAGGTCCTTTT | 1752 |
| Db | 1681 | CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGCGAGCTGCTCAGGTCCTTTT | 1740 |
| QY | 1753 | TGTCACGGAGACCACTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG | 1812 |
| Db | 1741 | TGTCACGGAGACCACTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG | 1800 |
| QY | 1813 | CAAGTTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGTTGACGTGGGGAGCTGTC | 1872 |
| Db | 1801 | CAAGTTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGTTGACGTGGGGAGCTGTC | 1860 |
| QY | 1873 | GGAAGCAGAGGTTCAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCG | 1932 |
| Db | 1861 | GGAAGCAGAGGTTCAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCG | 1920 |
| QY | 1933 | CTTTCATCCCCAAGCCTGACGGGCTGCGCGCATTTGAAATGGACTACGCTCGTGGGAGC | 1992 |
| Db | 1921 | CTTTCATCCCCAAGCCTGACGGGCTGCGCGCATTTGAAATGGACTACGCTCGTGGGAGC | 1980 |
| QY | 1993 | CAGAGCTTCCCGCAGAGAAAGAGGCGCGAGCTCTCACCTCAGAGGTTGAAGCACTGTT | 2052 |
| Db | 1981 | CAGAGCTTCCCGCAGAGAAAGAGGCGCGAGCTCTCACCTCAGAGGTTGAAGCACTGTT | 2040 |
| QY | 2053 | CAGCGTGTCACTACAGCGGGCGCGGCCCGCCCTGCTGGGCGCTCTGTGTGTGG | 2112 |
| Db | 2041 | CAGCGTGTCACTACAGCGGGCGCGGCCCGCCCTGCTGGGCGCTCTGTGTGTGG | 2100 |
| QY | 2113 | CTTGGAGCATATCCACAGGSCCTGGCGCACTTCTGCTGCTGCTGGGCGCCAGGACCC | 2172 |
| Db | 2101 | CTTGGAGCATATCCACAGGSCCTGGCGCACTTCTGCTGCTGCTGGGCGCCAGGACCC | 2160 |
| QY | 2173 | GCGGCTTACGCTGCTTCTCAAGGTGATGTGAGCGGCGCTAGACACCACTCCCGCA | 2232 |
| Db | 2161 | GCGGCTTACGCTGCTTCTCAAGGTGATGTGAGCGGCGCTAGACACCACTCCCGCA | 2220 |
| QY | 2233 | GGACAGGCTCACGGAGGTATCGCCAGCATCATCAAACCCCAAGAACACGTACTGCGTGG | 2292 |
| Db | 2221 | GGACAGGCTCACGGAGGTATCGCCAGCATCATCAAACCCCAAGAACACGTACTGCGTGG | 2280 |
| QY | 2293 | TGCGTATGCGGTGCTCCAGAGGCCCGCCATGGGACGCTCCGCAAGGCTTCAAGAGCCA | 2352 |
| Db | 2281 | TGCGTATGCGGTGCTCCAGAGGCCCGCCATGGGACGCTCCGCAAGGCTTCAAGAGCCA | 2340 |
| QY | 2353 | CGTCTTACCTTTCACAGACCTCCAGCGCTACATTCGACAGTTCGCTGCTCAGGAG | 2412 |
| Db | 2341 | CGTCTTACCTTTCACAGACCTCCAGCGCTACATTCGACAGTTCGCTGCTCAGGAG | 2400 |
| QY | 2413 | GACCAAGCCGCTGAGGATGCGCTGTCTATCGAGCAGAGCTCTCCCTGAATGAGGCCAG | 2472 |
| Db | 2401 | GACCAAGCCGCTGAGGATGCGCTGTCTATCGAGCAGAGCTCTCCCTGAATGAGGCCAG | 2460 |

2473 CAGTGGCTCTTCGACGCTCTTCTACGCTTCATGTGCGCCACACGCGCTGGCGCATCAGGG 2532
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2461 CAGTGGCTCTTCGACGCTCTTCTACGCTTCATGTGCGCCACACGCGCTGGCGCATCAGGG 2520
|||||
2533 CAAGTCTCAGTCCAGTCCAGGCGGATCCGCGAGGCTCCATCCTCTCCAGGCTGCTCTG 2592
|||||
2521 CAAGTCTCAGTCCAGTCCAGGCGGATCCGCGAGGCTCCATCCTCTCCAGGCTGCTCTG 2580
|||||
2593 CAGCTGTGCTAGGCGGACATGGAGAACAAAGCTTTTTCGGGGGATTCGGCGGAGCGGCT 2652
|||||
2581 CAGCTGTGCTAGGCGGACATGGAGAACAAAGCTTTTTCGGGGGATTCGGCGGAGCGGCT 2640
|||||
2653 GCTCTCGGTTTGGTGATGATTTCTTGGTGACACCTCACCTCACCCACGCGAAAC 2712
|||||
2641 GCTCTCGGTTTGGTGATGATTTCTTGGTGACACCTCACCTCACCCACGCGAAAC 2700
|||||
2713 CTTCTCAGGACCTGTGTCGAGGTGTCCTGAGTATGGCTGGTGGAACCTTGCAGAA 2772
|||||
2701 CTTCTCAGGACCTGTGTCGAGGTGTCCTGAGTATGGCTGGTGGAACCTTGCAGAA 2760
|||||
2773 GACAGTGGTGAACCTCCCTTAGAAGACGAGGCGCTGGTGGCAGCGCTTTTGTTCAGAT 2832
|||||
2761 GACAGTGGTGAACCTCCCTTAGAAGACGAGGCGCTGGTGGCAGCGCTTTTGTTCAGAT 2820
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2833 GCGGGCCACGCGCTATTCCTCTGGTGGCGCTGCTGCTGGATACCGGACCTCTGAGGT 2892
|||||
2821 GCGGGCCACGCGCTATTCCTCTGGTGGCGCTGCTGCTGGATACCGGACCTCTGAGGT 2880
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2893 GCAGAGGACTACTCCAGCTATGCCGCGACTCCATCAGAGCGAGTCTCACCTTCAACCG 2952
|||||
2881 GCAGAGGACTACTCCAGCTATGCCGCGACTCCATCAGAGCGAGTCTCACCTTCAACCG 2940
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2953 CGGCTTCAAGCTGGGAGGAACATGCTCGCAACTCTTTGGGCTCTTGGGCTGAAGTG 3012
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3013 TCACAGCTCTTCTTGATTTGAGGTGAACAGCTCCAGAGGCTGTCACCAACATCTA 3072
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3001 TCACAGCTCTTCTTGATTTGAGGTGAACAGCTCCAGAGGCTGTCACCAACATCTA 3060
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3073 CAAGATCTCTCTGTCGAGCGGTACAGGTTTACGAGTGTGCTGCGAGTCCCATTTCA 3132
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3061 CAAGATCTCTCTGTCGAGCGGTACAGGTTTACGAGTGTGCTGCGAGTCCCATTTCA 3120
|||||
3133 TCAGCAAGTTTGAAGAACCCACATTTTCTCGCGGTCTCTCTGACAGCGCTCCCT 3192
|||||
3121 TCAGCAAGTTTGAAGAACCCACATTTTCTCGCGGTCTCTCTGACAGCGCTCCCT 3180
|||||
3193 CTGCTACTCATCTGNAAGCCAGAACGAGGATGTCCTGGGGCCCAAGGCGCGCG 3252
|||||
3181 CTGCTACTCATCTGNAAGCCAGAACGAGGATGTCCTGGGGCCCAAGGCGCGCG 3240
|||||
3253 CGGCGCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3312
|||||
3241 CGGCGCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
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3313 GACTCGACACCGTGTCACTTACCTTACCTTCCCTCGCGGTCTCTGAGGCTACTCAGGACGCCAGAGCGCA 3372
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|||||
3361 GCTGAGTCGGAAGCTCCCGGGAGGAGGCTGACTGCTGGAGCGCGCACGCCAGCGCGC 3420
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RESULT 8

US-10-054-611-224

; Sequence 224, Application US/10054611

; Publication No. US20030059787A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. US20030059787A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/054,611

; FILING DATE: 18-Jan-2002

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/854,050

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 224:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4015 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hprt"
; /note= "human telomerase reverse
; transcriptase (hprt) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-611-224

Query Match 99.6%; Score 3784.4; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GCAGCGCTCCGCTGCTGCGACAGTGGGAAGCCCTGGCCCGCGCCACCCCGCGATGCC 72
DB 1 GCAGCGCTCCGCTGCTGCGACAGTGGGAAGCCCTGGCCCGCGCCACCCCGCGATGCC 60
QY 73 GCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 132
DB 61 GCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
QY 133 GCGCGTGGCCACGTTGTCGCGCGCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGGG 192
DB 121 GCGCGTGGCCACGTTGTCGCGCGCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGGG 180
QY 193 GGACCGCGCGCTTCCGCGCGCTGGTGCCGCCAGTGCCTGGTGTGGTGCCCTGGGAGGC 252
DB 181 GGACCGCGCGCTTCCGCGCGCTGGTGCCGCCAGTGCCTGGTGTGGTGCCCTGGGAGGC 240
QY 253 ACGGCGCGCCCGCGCGCCCTCCTTCCTCCGCGAGTGTCTCCTGGAAGAGCTGCTGCG 312
DB 241 ACGGCGCGCCCGCGCGCCCTCCTTCCTCCGCGAGTGTCTCCTGGAAGAGCTGCTGCG 300
QY 313 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGAAGACGTGCTGGCTTCGGCTTCGC 372
DB 301 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGAAGACGTGCTGGCTTCGGCTTCGC 360
QY 373 GCTGCTGGACGGGGCGCGGGGGCCCCCGCGAGGCTTCACACACAGGCTGCGGAGCTA 432
DB 361 GCTGCTGGACGGGGCGCGGGGGCCCCCGCGAGGCTTCACACACAGGCTGCGGAGCTA 420
QY 433 CTTGCCCAACACGCTGACCGAGCGACTGCGGGGAGCGGGGCTGCTGCTGCG 492
DB 421 CTTGCCCAACACGCTGACCGAGCGACTGCGGGGAGCGGGGCTGCTGCTGCG 480
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QY 613 TCAGCGCGGGCGCGCGCACACGCTAGTGGACCCCGAAGCGCTCTGGGATCGAAGCGG 672
DB 601 TCAGCGCGGGCGCGCGCACACGCTAGTGGACCCCGAAGCGCTCTGGGATCGAAGCGG 660
QY 673 CTGGAAACCATAGCTCAGGAGCGCGGGTCCCTGCTGGGCTGCCAGCGCGGGTCCGAG 732
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DB 841 GCGTGACCGAGTACCGTGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

QY 913 CACCTCTTTGGAGGGTGGCTCTCTGGGACGGCGGCACCTCCACCCATCCGTGGGCGGCCA 972
DB 901 CACCTCTTTGGAGGGTGGCTCTCTGGGACGGCGGCACCTCCACCCATCCGTGGGCGGCCA 960
QY 973 GCACACAGGGGCGCGCCCATCCACATCGCGGCGCACACGCTCCCTGGGACACGCTTGTCC 1032
DB 961 GCACACAGGGGCGCGCCCATCCACATCGCGGCGCACACGCTCCCTGGGACACGCTTGTCC 1020
QY 1033 CCCGCTGTACGCCGAGACCAACACATCTCTACTCTCTCAGGCGACAAGAGCAGCTGGC 1092
DB 1021 CCCGCTGTACGCCGAGACCAACACATCTCTACTCTCAGGCGACAAGAGCAGCTGGC 1080
QY 1093 GCGCTCTTCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGCGGTCTGGAGGCTCTGTGA 1152
DB 1081 GCGCTCTTCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGCGGTCTGGAGGCTCTGTGA 1140
QY 1153 GACCATCTTCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT 1212
DB 1141 GACCATCTTCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT 1200
QY 1213 GCGCAGCGCTACTGGCAAAATCGGCGCCTGTTTCTGAGCTGCTTGGAAACACACGCA 1272
DB 1201 GCGCAGCGCTACTGGCAAAATCGGCGCCTGTTTCTGAGCTGCTTGGAAACACACGCA 1260
QY 1273 GTGCCCTACGGGTTGCTCTCAAGACGACTGCGCGCTGCGAGCTGCGGTCACCCCAGC 1332
DB 1261 GTGCCCTACGGGTTGCTCTCAAGACGACTGCGCGCTGCGAGCTGCGGTCACCCCAGC 1320
QY 1333 AGCGGTGCTGTGCGCGGAGAACCCAGGGCTCTGTGGCGGCCCGCGAGGAGGA 1392
DB 1321 AGCGGTGCTGTGCGCGGAGAACCCAGGGCTCTGTGGCGGCCCGCGAGGAGGA 1380
QY 1393 CACAGACCCCTGCGCTGGTGTGCTGCTGCCAGCAGACAGAGCCCTTGGCAGGTGTA 1452
DB 1381 CACAGACCCCTGCGCTGGTGTGCTGCCAGCAGACAGAGCCCTTGGCAGGTGTA 1440
QY 1453 CGGCTCTGCGGGGCTGCTGCGCGGCTGCTGCGCGGCTGCTGCGGCTCTGGGCTCCAGGA 1512
DB 1441 CGGCTCTGCGGGGCTGCTGCGCGGCTGCTGCGCGGCTGCTGCGGCTCTGGGCTCCAGGA 1500
QY 1513 CAACGAACCGCTCTCTCAGGAACACCAAGAAATTCATCTCCTGGGAAAGCATCCCAA 1572
DB 1501 CAACGAACCGCTCTCTCAGGAACACCAAGAAATTCATCTCCTGGGAAAGCATCCCAA 1560
QY 1573 GCTCTGCTGCGAGGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGGCTGCGCAG 1632
DB 1561 GCTCTGCTGCGAGGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGGCTGCGCAG 1620
QY 1633 GAGCCAGGGTTGGCTGTGTTCCGCGCGCAGACACCGCTCTGCTGAGGAGATCCTGGC 1692
DB 1621 GAGCCAGGGTTGGCTGTGTTCCGCGCGCAGACACCGCTCTGCTGAGGAGATCCTGGC 1680
QY 1693 CAAGTTCTTCTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752
DB 1681 CAAGTTCTTCTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1753 TGTACCGGAGACCGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1812
DB 1741 TGTACCGGAGACCGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
QY 1813 CAAGTTGCAAGCATTTGGAATCAGACAGCATTGAAGAGGTTGACGCTCGGGAGGTGTC 1872
DB 1801 CAAGTTGCAAGCATTTGGAATCAGACAGCATTGAAGAGGTTGACGCTCGGGAGGTGTC 1860
QY 1873 GGAACGAGGTCAGGACATCGGGAAGCCAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1932
DB 1861 GGAACGAGGTCAGGACATCGGGAAGCCAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
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DB 1921 CTTATCCCAAGCCTGACGGCTGCGGCGGCTGTTGAAACATGAGACTAGCTGCTGGGAGC 1980

QY 1993 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACGTGT 2052
Db 1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACGTGT 2040
QY 2053 CAGCGTCTCAACTACAGCGGGCGGGCGGCCCGCGCTCTCTGGCGCCCTCTGTGCTGGG 2112
Db 2041 CAGCGTCTCAACTACAGCGGGCGGGCGGCCCGCGCTCTCTGGCGCCCTCTGTGCTGGG 2100
QY 2113 CTGGAGGATATCCACAGGCGCTGGGCGACCTTCTGCTGCTGCGTGGGCGCCACGAGACCC 2172
Db 2101 CTGGAGGATATCCACAGGCGCTGGGCGACCTTCTGCTGCTGCGTGGGCGCCACGAGACCC 2160
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QY 2473 CAGTGGCCTCTCGACGTCTTCTTACGCTTCATGTGCCACACGCGCTGGCGCATCAGGGG 2532
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QY 2533 CAAGTCTTACGTCCAGTCCAGGGATCCCGCAGGGCTCATCTCTCCAGCTGCTCTG 2592
Db 2521 CAAGTCTTACGTCCAGTCCAGGGATCCCGCAGGGCTCATCTCTCCAGCTGCTCTG 2580
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Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAACTCTTTGGGTCTTGGCGCTGAAGTG 3000
QY 3013 TCACAGCGTGTCTTGATTTGACGGTGAACAGCCCTCCAGACGGTGTGACCAACATCTA 3072
Db 3001 TCACAGCGTGTCTTGATTTGACGGTGAACAGCCCTCCAGACGGTGTGACCAACATCTA 3060
QY 3073 CAAGATCCCTCTCTCGAGCGGTACAGGTTTCAGGCATGTGCTGCAGGCTCCCATTTCA 3132

Db 3061 CAAGATCCCTCTCTGTCAGGCGTACAGGTTTACGCATGTGTGTCAGCTCCCATTTCA 3120
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Db 3361 GCTGAGTCTGGAAGCTCCCGGGGACGAGCTGACTGCGCTGGAGGCGCAGCCAAACCGCGC 3420
QY 3433 ACTGCGCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGGCGCA 3492
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QY 3793 CCTGAT 3798
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RESULT 9
US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015

;
TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

Query Match 99.6%; Score 3784.4; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| QY | 73 | GCGCGCTCCCGCTGCCGAGCGCTGCGCTCCCTGCTGGCGAGCCACTACCGGAGGTGCT | 132 |
| DB | 61 | GCGCGCTCCCGCTGCCGAGCGCTGCGCTCCCTGCTGGCGAGCCACTACCGGAGGTGCT | 120 |
| QY | 133 | GCGCGTGGCCAGCTTCGTGCGGCGCTTGGGCGCCAGGGCTGGCGGCTGGTCAGCGGGG | 192 |
| DB | 121 | GCGCGTGGCCAGCTTCGTGCGGCGCTTGGGCGCCAGGGCTGGCGGCTGGTCAGCGGGG | 180 |
| QY | 193 | GGACCCGCGCGCTTCCGCGCGCTGGTGGCCCACTGCTGTGTGCTGCCCTGGGACGC | 252 |
| DB | 181 | GGACCCGCGCGCTTCCGCGCGCTGGTGGCCCACTGCTGTGTGCTGCCCTGGGACGC | 240 |
| QY | 253 | ACGGCGCGCCCGCGCGCCCTCCCTTCGCGCAGGTGCTGCTGCCCTGAAGAGCTGGTGC | 312 |
| DB | 241 | ACGGCGCGCCCGCGCGCCCTCCCTTCGCGCAGGTGCTGCTGCCCTGAAGAGCTGGTGC | 300 |
| QY | 313 | CGAGTGTGTCAGAGGCTGTGGGAGCGGCGGCGGAGAACGTGCTGGCTTCGGCTTCGC | 372 |
| DB | 301 | CGAGTGTGTCAGAGGCTGTGGGAGCGGCGGCGGAGAACGTGCTGGCTTCGGCTTCGC | 360 |
| QY | 373 | GCTGCTGGACGGGCGCGGGGCGCCCGCGAGGCTTACACACAGCGTGCAGACTA | 432 |
| DB | 361 | GCTGCTGGACGGGCGCGGGGCGCCCGCGAGGCTTACACACAGCGTGCAGACTA | 420 |
| QY | 433 | CTGTCCCAACACCGTGAACGACACTGCGGGGAGCGGGGCTGGGGCTGCTGCTGG | 492 |
| DB | 421 | CTGTCCCAACACCGTGAACGACACTGCGGGGAGCGGGGCTGGGGCTGCTGCTGG | 480 |
| QY | 493 | CGCGTGGCGGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 552 |
| DB | 481 | CGCGTGGCGGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 540 |
| QY | 553 | GGCTCCCACTGCGCTTACCAAGTGTGGGGCGCGCTGTACCAAGCTCGGGCGTGCAC | 612 |
| DB | 541 | GGCTCCCACTGCGCTTACCAAGTGTGGGGCGCGCTGTGTACCAAGCTCGGGCGTGCAC | 600 |
| QY | 613 | TCAGCCCG | 672 |
| DB | 601 | TCAGCCCG | 660 |
| QY | 673 | CTGGAAACATACGCTCAGGAGCGCGGGTCCCGCTGGCGCTGCCAGCCCGCGGTCGAG | 732 |
| DB | 661 | CTGGAAACATACGCTCAGGAGCGCGGGTCCCGCTGGCGCTGCCAGCCCGCGGTCGAG | 720 |
| QY | 733 | GAGGCGGGGCGAGTGCACCGCAAGTGTGCGCGTGGCCAGAGGCGCCAGCGTGGCG | 792 |
| DB | 721 | GAGGCGGGGCGAGTGCACCGCAAGTGTGCGCGTGGCCAGAGGCGCCAGCGTGGCG | 780 |
| QY | 793 | TGCGCCTGAGCGGAGCGAGCCCGCTGGGCGAGGGTCTTGGGCGCCAGCGCGAGGAC | 852 |
| DB | 781 | TGCGCCTGAGCGGAGCGAGCCCGCTGGGCGAGGGTCTTGGGCGCCAGCGCGAGGAC | 840 |
| QY | 853 | GCGTGGACCGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 912 |
| DB | 841 | GCGTGGACCGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 900 |
| QY | 913 | CACCTCTTTGGAGGGTGGCTCTCTGGACAGCGGCCACTCCCAACCCATCCGTGGGCGGCA | 972 |

| | | | |
|----|------|---|------|
| DB | 901 | CACCTCTTTGGAGGGTGGCTCTCTGGACAGCGGCCACTCCCAACCATCCGTGGGCGGCA | 960 |
| QY | 973 | GCACACGCGGCG | 1032 |
| DB | 961 | GCACACGCGGCG | 1020 |
| QY | 1033 | CCCGGTGTACGCGGAGACCAAGCACTTCCTCTACTCTCTAGGCGCAAGGAGCAGTGG | 1092 |
| DB | 1021 | CCCGGTGTACGCGGAGACCAAGCACTTCCTCTACTCTCTAGGCGCAAGGAGCAGTGG | 1080 |
| QY | 1093 | GCCCTCTCTCTACTCAGCTCTCTAGGCGCCAGCTGCTGCGCTGCGAGGCTCTGTGA | 1152 |
| DB | 1081 | GCCCTCTCTCTACTCAGCTCTCTAGGCGCCAGCTGCTGCGCTGCGAGGCTCTGTGA | 1140 |
| QY | 1153 | GACCATCTTTCTGGGTTCAGGCCCTTGATGCCAGGACTCCCGCAGGTTGCCCGCCT | 1212 |
| DB | 1141 | GACCATCTTTCTGGGTTCAGGCCCTTGATGCCAGGACTCCCGCAGGTTGCCCGCCT | 1200 |
| QY | 1213 | GCCCCAGCGCTACTGGCAATGGGCCCTGTTTCTGGAGCTGCTTGGGAACACCGCA | 1272 |
| DB | 1201 | GCCCCAGCGCTACTGGCAATGGGCCCTGTTTCTGGAGCTGCTTGGGAACACCGCA | 1260 |
| QY | 1273 | GTGCCCTACGCGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCAACCCAG | 1332 |
| DB | 1261 | GTGCCCTACGCGGTGCTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCAACCCAG | 1320 |
| QY | 1333 | AGCCGGTGTCTGTGCCCGGAGAACCCAGGGCTCTGTGGCGGCCCGCGAGGAGGA | 1392 |
| DB | 1321 | AGCCGGTGTCTGTGCCCGGAGAACCCAGGGCTCTGTGGCGGCCCGCGAGGAGGA | 1380 |
| QY | 1393 | CACAGACCCCGCTGCGCTGGTGCAGTGTCTGCCAGACAGCAGAGCCCTGGCAGTGT | 1452 |
| DB | 1381 | CACAGACCCCGCTGCGCTGGTGCAGTGTCTGCCAGACAGCAGAGCCCTGGCAGTGT | 1440 |
| QY | 1453 | CGGCTTCGTGCGGGCTGCTGCGCGCTGTGCGCCAGCGCTCTGGGCTTCCAGGCA | 1512 |
| DB | 1441 | CGGCTTCGTGCGGGCTGCTGCGCGCTGTGCGCCAGCGCTCTGGGCTTCCAGGCA | 1500 |
| QY | 1513 | CAACGAACCGCTTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA | 1572 |
| DB | 1501 | CAACGAACCGCTTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA | 1560 |
| QY | 1573 | GCTCTGCTGCGAGGAGTGCAGTGGAGATGAGCGTGGCGGAGTGGCTGGCGAG | 1632 |
| DB | 1561 | GCTCTGCTGCGAGGAGTGCAGTGGAGATGAGCGTGGCGGAGTGGCTGGCGAG | 1620 |
| QY | 1633 | GAGCCAGGGTGGCTGTTCGCGCGCAGAGCACCGCTGCTGCGTGAGGAGATCCTGC | 1692 |
| DB | 1621 | GAGCCAGGGTGGCTGTTCGCGCGCAGAGCACCGCTGCTGCGTGAGGAGATCCTGC | 1680 |
| QY | 1693 | CAAGTTCCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG | 1752 |
| DB | 1681 | CAAGTTCCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG | 1740 |
| QY | 1753 | TGTCAGGAGACCAAGTTCCTCAAGAACAGGCTCTTTTCTACCGGAAGATGCTGGAG | 1812 |
| DB | 1741 | TGTCAGGAGACCAAGTTCCTCAAGAACAGGCTCTTTTCTACCGGAAGATGCTGGAG | 1800 |
| QY | 1813 | CAAGTTCCTCAAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATG | 1872 |
| DB | 1801 | CAAGTTCCTCAAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATG | 1860 |
| QY | 1873 | GGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCGCGCTGCTGCTGCTGCTGCTG | 1932 |
| DB | 1861 | GGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCGCGCTGCTGCTGCTGCTGCTG | 1920 |
| QY | 1933 | CTTCTATCCCAAGCGCTGAGCGGCTGCGCGGATGTGAACATGGACTACGCTCGTGGAGC | 1992 |
| DB | 1921 | CTTCTATCCCAAGCGCTGAGCGGCTGCGCGGATGTGAACATGGACTACGCTCGTGGAGC | 1980 |
| QY | 1993 | CAGACGTTCCCGCAGAGAAAGAGGCGCGAGGCTCTACCTCGAGGGTGAAGGCACTGTT | 2052 |

Db 1981 CAGAACGTTCCGACAGAAAAAGAGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040
QY 2053 CAGCGTCTCAACTACAGAGGGGGCGGGCCCGCGCTCTCTGGCGCCCTCTGTCGTGGG 2112
Db 2041 CAGCGTCTCAACTACAGAGGGGGCGGGCCCGCGCTCTCTGGCGCCCTCTGTCGTGGG 2100
QY 2113 CCTGGAGATATCCACAGGCGCTGGCGCACTTCTGCTGGTGGTGGGGCCCGAGGACCC 2172
Db 2101 CCTGGAGATATCCACAGGCGCTGGCGCACTTCTGCTGGTGGTGGGGCCCGAGGACCC 2160
QY 2173 GCGCCCTGAGCTGTACTTTGTCAGGTGGATGTGACGGGGCGGTACGACACCACTTCCCCCA 2232
Db 2161 GCGCCCTGAGCTGTACTTTGTCAGGTGGATGTGACGGGGCGGTACGACACCACTTCCCCCA 2220
QY 2233 GGACAGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAACACGACTGCTGCGTGG 2292
Db 2221 GGACAGCTCAGGAGGTATCGCCAGCATATCAAAACCCAGAACACGACTGCTGCGTGG 2280
QY 2293 TCGGTATGCGGTGTCAGAGGCCCGCCATGGCAGCTCGCAAGGCCCTTCAAGAGCCA 2352
Db 2281 TCGGTATGCGGTGTCAGAGGCCCGCCATGGCAGCTCGCAAGGCCCTTCAAGAGCCA 2340
QY 2353 CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCAGGA 2412
Db 2341 CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCAGGA 2400
QY 2413 GACCAAGCCCTGAGGATCCGTCGTATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG 2472
Db 2401 GACCAAGCCCTGAGGATCCGTCGTATCGAGCAGAGTCTCTCCCTGAATGAGGCCAG 2460
QY 2473 CAGTGGGCTCTTCGACGCTCTTCAGCTTCATGCTGTCACACCGCGCTGCGCATCAGGG 2532
Db 2461 CAGTGGGCTCTTCGACGCTCTTCAGCTTCATGCTGTCACACCGCGCTGCGCATCAGGG 2520
QY 2533 CAAGTCTCTACCTCCAGTCCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG 2592
Db 2521 CAAGTCTCTACCTCCAGTCCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG 2580
QY 2593 CAGCCTGTGTCAGCGGACATGAGAACAAAGCTGTTTGGGGGATTCGGGGGACGGGCT 2652
Db 2581 CAGCCTGTGTCAGCGGACATGAGAACAAAGCTGTTTGGGGGATTCGGGGGACGGGCT 2640
QY 2653 GCTCCTCGCTTGGTGATATTTCTGTTGGTGACACCTCACTCAACCCACGCAAAAC 2712
Db 2641 GCTCCTCGCTTGGTGATATTTCTGTTGGTGACACCTCACTCAACCCACGCAAAAC 2700
QY 2713 CTTCCTCAGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGGTGAACCTTGGGAA 2772
Db 2701 CTTCCTCAGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGGTGAACCTTGGGAA 2760
QY 2773 GACAGTGGTGAACCTTCCTGTAGAACGAGGCCCTGGGGGACGGCTTTTGTTCAGAT 2832
Db 2761 GACAGTGGTGAACCTTCCTGTAGAACGAGGCCCTGGGGGACGGCTTTTGTTCAGAT 2820
QY 2833 GCGGGCCAGGGCTATTCCTCCGTGGCGCTGCTGCTGATACCGGACCTGGAGGT 2892
Db 2821 GCGGGCCAGGGCTATTCCTCCGTGGCGCTGCTGCTGATACCGGACCTGGAGGT 2880
QY 2893 GCAGAGGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2952
Db 2881 GCAGAGGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
QY 2953 CGCGTTCAGGCTGGGAGAACATGCGTGCAAACTCTTTGGGGCTTGGGGCTGAAGTG 3012
Db 2941 CGCGTTCAGGCTGGGAGAACATGCGTGCAAACTCTTTGGGGCTTGGGGCTGAAGTG 3000
QY 3013 TCACAGCTGTTTCTGATTTGAGGTGACGTGACAGCTCCAGACGGTGTGACCAACATCTA 3072
Db 3001 TCACAGCTGTTTCTGATTTGAGGTGACGTGACAGCTCCAGACGGTGTGACCAACATCTA 3060
QY 3073 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCGATGTGCTGCAGCTCCCATTTCA 3132
Db 3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCGATGTGCTGCAGCTCCCATTTCA 3120

QY 3133 TCACAAAGTTTGGAAAGAACCCCACTTTTCTCTGGCGTCACTCTCTGACAGGGCTCCCT 3192
Db 3121 TCACAAAGTTTGGAAAGAACCCCACTTTTCTCTGGCGTCACTCTCTGACAGGGCTCCCT 3180
QY 3193 CTGCTACTCCATCTCTGAAGCCAAAGAACGAGGATGCTGCTGGGGCCCAAGGGCGCGC 3252
Db 3181 CTGCTACTCCATCTCTGAAGCCAAAGAACGAGGATGCTGCTGGGGCCCAAGGGCGCGC 3240
QY 3253 CCGCCCTCTGCCCCTCCGAGGCCGTGACGTGGCTGTGCCAACCAAGCATTTCTGTCTCAAGCT 3312
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QY 3313 GACTCGACACCGTGTCACTTACGTGCGACCTCTCTGGGTCACTCAGGACAGCCAGAGCGCA 3372
Db 3301 GACTCGACACCGTGTCACTTACGTGCGACCTCTCTGGGTCACTCAGGACAGCCAGAGCGCA 3360
QY 3373 GCTGAGTCSGNAAGTCCCGGGGAGCGCTGACTGCGCTGGAGGCCGACGCAACCCGCGC 3432
Db 3361 GCTGAGTCSGNAAGTCCCGGGGAGCGCTGACTGCGCTGGAGGCCGACGCAACCCGCGC 3420
QY 3433 ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGGCGCA 3492
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGGCGCA 3480
QY 3493 GAGCAGACACAGAGCCCTGTACGCCGGGCTCTACGTCCCAAGGAGGAGGGCGCGCC 3552
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QY 3553 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCTGAGTGGTGGTGGCGAGGCGCTG 3612
Db 3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCTGAGTGGTGGTGGCGAGGCGCTG 3600
QY 3613 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3672
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3660
QY 3673 GAGTGTCCAGCACACCTGCGCTTCTACTTCCCCACAGGCTGGGCTCGGCTCCACCCCA 3732
Db 3661 GAGTGTCCAGCACACCTGCGCTTCTACTTCCCCACAGGCTGGGCTCGGCTCCACCCCA 3720
QY 3733 GGGCAGCTTTTCTCTACAGGAGGCCGCTTCCACTCCCCACATAGAAATAGTCCATCC 3792
Db 3721 GGGCAGCTTTTCTCTACAGGAGGCCGCTTCCACTCCCCACATAGAAATAGTCCATCC 3780
QY 3793 CCTGAT 3798
Db 3781 CCAGAT 3786

RESULT 10

US-10-044-692-1
; Sequence 1, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/044,692
 ; FILING DATE: 11-Jan-2002
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/912,951
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002600US

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 4015 base pairs
 ; TYPE: nucleic acid

; STRANDEDNESS: single
 ; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS
 ; LOCATION: 56..3454

; OTHER INFORMATION: /product= "hprt"
 ; /note= "human telomerase reverse

; transcriptase (hprt) catalytic protein
 ; component"

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-044-692-1

Query Match 99.6%; Score 3784.4; DB 14; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|----|-----|---|-----|
| QY | 13 | GCAGCGCTGCCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCCACCCCGCGATGCC | 72 |
| Db | 1 | GCAGCGCTGCCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCCACCCCGCGATGCC | 60 |
| QY | 73 | CGCGGCTCCCGCTGCCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT | 132 |
| Db | 61 | CGCGGCTCCCGCTGCCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT | 120 |
| QY | 133 | CGCGGTGCCACGTTCTGTCGCGCGCTGGGCCCCAGGGCTGGCGGTGGTGCACGCGGG | 192 |
| Db | 121 | CGCGGTGCCACGTTCTGTCGCGCGCTGGGCCCCAGGGCTGGCGGTGGTGCACGCGGG | 180 |
| QY | 193 | GGACCCGGCGGCTTCCCGCGGCTGGTGGCCAGTGCCTGGTGGCTGGCGCTGGGAGCG | 252 |
| Db | 181 | GGACCCGGCGGCTTCCCGCGGCTGGTGGCCAGTGCCTGGTGGCTGGCGCTGGGAGCG | 240 |
| QY | 253 | ACGGCGCGCCCGCGCGCCCTCTCTCCGCGAGTGTCTTGAAGAGCTGGTGGC | 312 |
| Db | 241 | ACGGCGCGCCCGCGCGCCCTCTCTCCGCGAGTGTCTTGAAGAGCTGGTGGC | 300 |
| QY | 313 | CCGAGTGTGAGAGGCTGTGCGAGCGCGCGGCGAAGACGTGTGGCTTCGGCTTCGC | 372 |
| Db | 301 | CCGAGTGTGAGAGGCTGTGCGAGCGCGCGGCGAAGACGTGTGGCTTCGGCTTCGC | 360 |

| | | | |
|----|------|--|------|
| QY | 373 | GCTGCTGACGGGGCCCGGGGGCCCGCCCGAGGCGCTTACACACAGGTGCGCAGCTA | 432 |
| Db | 361 | GCTGCTGACGGGGCCCGGGGGCCCGCCCGAGGCGCTTACACACAGGTGCGCAGCTA | 420 |
| QY | 433 | CCTGCCAACACAGGTGACCGAGCACTGCGGGGGAGCGGGGCTGGGGCTCTCTCTCGG | 492 |
| Db | 421 | CCTGCCAACACAGGTGACCGAGCACTGCGGGGGAGCGGGGCTGGGGCTCTCTCTCGG | 480 |
| QY | 493 | CGCGTGGCGGACGAGCTGCTGGTTACCTGCTGCACGCTCGCGGCTCTTTGTGCTGGT | 552 |
| Db | 481 | CGCGTGGCGGACGAGCTGCTGGTTACCTGCTGCACGCTCGCGGCTCTTTGTGCTGGT | 540 |
| QY | 553 | GGCTCCAGCTGCGGCTACACAGTGTGGGGCCCGCTGTACCAAGCTCGGGCTCTGGC | 612 |
| Db | 541 | GGCTCCAGCTGCGGCTACACAGTGTGGGGCCCGCTGTACCAAGCTCGGGCTCTGGC | 600 |
| QY | 613 | TCAGCGCGCGCCCGCCACAGCTAGTGGAGCCCGAAGGCTCTGGATGGAACAGGCG | 672 |
| Db | 601 | TCAGCGCGCGCCCGCCACAGCTAGTGGAGCCCGAAGGCTCTGGATGGAACAGGCG | 660 |
| QY | 673 | CTGGAACCATAGCGTCAGGAGGCGGGGTCCTGGGCTGCGAGCCCGGGTGGAG | 732 |
| Db | 661 | CTGGAACCATAGCGTCAGGAGGCGGGGTCCTGGGCTGCGAGCCCGGGTGGAG | 720 |
| QY | 733 | GAGCGCGGGGCACTGCCAGCGAAGTCTGCGCTTGCCTGCCAAGAGGCGCGGCGC | 792 |
| Db | 721 | GAGCGCGGGGCACTGCCAGCGAAGTCTGCGCTTGCCTGCCAAGAGGCGCGGCGC | 780 |
| QY | 793 | TGCCCCCTGAGCGGAGCGAGCCCGCTTGGGAGGGGCTCTGGGCGCCACCCGGGAGG | 852 |
| Db | 781 | TGCCCCCTGAGCGGAGCGAGCCCGCTTGGGAGGGGCTCTGGGCGCCACCCGGGAGG | 840 |
| QY | 853 | GGTGGACCGAGTACCGTGGTTCTGTGTGTGTACCTGCCAGACCGCGCGAAGAAC | 912 |
| Db | 841 | GGTGGACCGAGTACCGTGGTTCTGTGTGTGTACCTGCCAGACCGCGCGAAGAAC | 900 |
| QY | 913 | CACCTCTTTGGAGGCTGCGCTCTGCGACGCGCCACTCCACCCATCCGTGGGCGGCA | 972 |
| Db | 901 | CACCTCTTTGGAGGCTGCGCTCTGCGACGCGCCACTCCACCCATCCGTGGGCGGCA | 960 |
| QY | 973 | GCACACGCGGGCCCGCCATCCACATCGCGGCGCACAGTCCCTGGGACACGCCCTTGC | 1032 |
| Db | 961 | GCACACGCGGGCCCGCCATCCACATCGCGGCGCACAGTCCCTGGGACACGCCCTTGC | 1020 |
| QY | 1033 | CCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGCGGACAAAGGAGCAGTGG | 1092 |
| Db | 1021 | CCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGCGGACAAAGGAGCAGTGG | 1080 |
| QY | 1093 | GCCCTCTCTTACTTACTCTCTCAGGCGGACCGCTGACTGCGGCTCGGAGGCTGTGA | 1152 |
| Db | 1081 | GCCCTCTCTTACTTACTCTCTCAGGCGGACCGCTGACTGCGGCTCGGAGGCTGTGA | 1140 |
| QY | 1153 | GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTCCCGCGCT | 1212 |
| Db | 1141 | GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTCCCGCGCT | 1200 |
| QY | 1213 | GCCCCAGCGCTACTTGGCAAAATGCGGCCCTCTTCTTGGAGCTGTCTGGGAAACACG | 1272 |
| Db | 1201 | GCCCCAGCGCTACTTGGCAAAATGCGGCCCTCTTCTTGGAGCTGTCTGGGAAACACG | 1260 |
| QY | 1273 | GTGCCCCCTACGGGGTGTCTTCAAGACGACTGCGCGCTGCGAGTGGGGTCAACCCAGC | 1332 |
| Db | 1261 | GTGCCCCCTACGGGGTGTCTTCAAGACGACTGCGCGCTGCGAGTGGGGTCAACCCAGC | 1320 |
| QY | 1333 | AGCGGCTGTCTGTGCCCGGAGAACCCAGGGCTGTGTGGGGGCCCCGAGGAGGAGA | 1392 |
| Db | 1321 | AGCGGCTGTCTGTGCCCGGAGAACCCAGGGCTGTGTGGGGGCCCCGAGGAGGAGA | 1380 |
| QY | 1393 | CACAGACCCCGCTGCCCTGGTGTGAGTGTCTGCCAGACACAGCAGCCCTTGGCAGTGA | 1452 |
| Db | 1381 | CACAGACCCCGCTGCCCTGGTGTGAGTGTCTGCCAGACACAGCAGCCCTTGGCAGTGA | 1440 |
| QY | 1453 | CGGCTTCTGTGGGGGCTGCTGCGCGGCGGCTGTGGTGGCCCGAGGCGCTTCCAGGCA | 1512 |

QY 3673 GAGTGTCCAGACACTGCGCTTCACTTCCACAGAGCTGGCGCTGGCTCCACCCCA 3732
Db |||||
QY 3661 GAGTGTCCAGACACTGCGCTTCACTTCCACAGAGCTGGCGCTGGCTCCACCCCA 3720
Db |||||
QY 3733 GGGCCAGCTTTTCTCCACAGGAGCGCGCTTCCACTCCCAATAGTATCCATCC 3792
Db |||||
QY 3721 GGGCCAGCTTTTCTCCACAGGAGCGCGCTTCCACTCCCAATAGTATCCATCC 3780
QY 3793 CCTGAT 3798
Db || |||
QY 3781 CCAGAT 3786
Db || |||
RESULT 11
US-10-044-539-1
; Sequence 1, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hprt"
; /note= "human telomerase reverse
; transcriptase (hprt) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1

Query Match 99.6%; Score 3784.4; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 GCAGCGCTGGCTCTGCTGGCAGCTGGGAGCCCTGGCCCCCGCCACCCCGCGATGCC 72
Db |||||
QY 1 GCAGCGCTGGCTCTGCTGGCAGCTGGGAGCCCTGGCCCCCGCCACCCCGCGATGCC 60
Db |||||
QY 73 GGGCGCTCCCGCTGCGGAGCGCTGCTCCCTGCTGCGCAGCAGCTACCGCGAGGTGCT 132
Db |||||
QY 61 GGGCGCTCCCGCTGCGGAGCGCTGCTCCCTGCTGCGCAGCAGCTACCGCGAGGTGCT 120
Db |||||
QY 133 GCGCTGGCCACGTTCTGCGCGCTGGGGCCCGCCAGGGCTGGCGCTGGTGCAGCGCG 192
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QY 121 GCGCTGGCCACGTTCTGCGCGCTGGGGCCCGCCAGGGCTGGCGCTGGTGCAGCGCG 180
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QY 193 GGACCGGGGGCTTTCCGGCGCTGGTGGCCAGTGCCTGGTGGTGGTGGTGGTGGTGG 252
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QY 181 GGACCGGGGGCTTTCCGGCGCTGGTGGCCAGTGCCTGGTGGTGGTGGTGGTGGTGG 240
Db |||||
QY 253 AGGGCGCGCCCGCGCGCGCTTCCGCGCAGGTGCTGCTGCTGAAGAGAGTGGTGGC 312
Db |||||
QY 241 AGGGCGCGCCCGCGCGCGCTTCCGCGCAGGTGCTGCTGCTGAAGAGAGTGGTGGC 300
Db |||||
QY 313 CCGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGAAGAGCTGCTGGCTTCCGCTTCGC 372
Db |||||
QY 301 CCGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGAAGAGCTGCTGGCTTCCGCTTCGC 360
Db |||||
QY 373 GCTGTGGAGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGG 432
Db |||||
QY 361 GCTGTGGAGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGG 420
Db |||||
QY 433 CTGCGCCAAACACGGTGACGACGCTGCGGGGGAGCGGGGGCGGGGGCGGGGGCGGG 492
Db |||||
QY 421 CTGCGCCAAACACGGTGACGACGCTGCGGGGGAGCGGGGGCGGGGGCGGGGGCG 480
Db |||||
QY 493 CCGCTGGCGCAGCAGCTGCTGTTTCACTGTGGCAGCGCTGGCGCTCTTTGTGTGGT 552
Db |||||
QY 481 CCGCTGGCGCAGCAGCTGCTGTTTCACTGTGGCAGCGCTGGCGCTCTTTGTGTGGT 540
Db |||||
QY 553 GGTCTCCAGTGGCGCTTACAGGTGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCG 612
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QY 541 GGTCTCCAGTGGCGCTTACAGGTGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCG 600
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QY 613 TCAGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 672
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QY 601 TCAGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 660
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QY 673 CTGGAACCATAGGTCAGGGAGCGGGGGTCCCGCTGGGGCTGCCAGCCCCGGGTGGAG 732
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QY 733 GAGGCGGGGGCGAGTCCAGCGAGTGTGCGGTGGTGGTGGTGGTGGTGGTGGTGG 792
Db |||||
QY 721 GAGGCGGGGGCGAGTCCAGCGAGTGTGCGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Db |||||
QY 793 TGCCCTGAGCGGAGCGGCGGCTGGGCGAGGGTCTGGGGCGGGCGGGCGGGCGGG 852
Db |||||
QY 781 TGCCCTGAGCGGAGCGGCGGCTGGGCGAGGGTCTGGGGCGGGCGGGCGGGCGGG 840
Db |||||
QY 853 GCGTGACCGAGTGACCGTGGTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 912
Db |||||
QY 841 GCGTGACCGAGTGACCGTGGTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db |||||

| | | | | | | | |
|----|------|--|------|------|---|--|------|
| QY | 913 | CACCTCTTTGGAGGGTGGCTCTCTGTGCACGCGCCACTCCACCCATCCCGTGGCGCGCCA | 972 | 1981 | CAGAACSTTTCCGACAGAAAAGAGGCCGAGCGGTCTCACTCTGAGGGTGAAGCACTGTT | 2044 | |
| Db | 901 | CACCTCTTTGGAGGGTGGCTCTCTGTGCACGCGCCACTCCACCCATCCCGTGGCGCGCCA | 960 | QY | 2053 | CACGCTGTCTAACTACGACGGGCGCGCGCCCGCGCTCTCACTCTGTGTGCTGGG | 2112 |
| QY | 973 | GCACACGGGGCCCCCATCCACATCGCGGCGCACACAGTCCCTTGGGACACGCTTGTTC | 1032 | Db | 2041 | CACGCTGTCTAACTACGACGGGCGCGCGCCCGCGCTCTCTGTGTGCTGGG | 2100 |
| Db | 961 | GCACACGGGGCCCCCATCCACATCGCGGCGCACACAGTCCCTTGGGACACGCTTGTTC | 1020 | QY | 2113 | CTTGGACAGATATCCACAGAGGCTGGCGCACCTTCGTGTCTGCTGTGCTGGGGCCAGACCC | 2172 |
| QY | 1033 | CCCGGTGTAGCCGAGACCAAGCACTTCCCTCTACTCTCAGGCGACAAAGAGCAGTGGG | 1092 | Db | 2101 | CTTGGACAGATATCCACAGAGGCTTGGCGCACCTTCGTGTCTGCTGTGCTGGGGCCAGACCC | 2160 |
| Db | 1021 | CCCGGTGTAGCCGAGACCAAGCACTTCCCTCTACTCTCAGGCGACAAAGAGCAGTGGG | 1080 | QY | 2173 | GCCGCTGTAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGGTAGCACACCATCCCCA | 2232 |
| QY | 1093 | GCCCTCTTCTACTCAAGTCTCTGTAGGCCCAAGCTGACTGTGGGCTCGGAGGCTCTGGA | 1152 | Db | 2161 | GCCGCTGTAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGGTAGCACACCATCCCCA | 2220 |
| Db | 1081 | GCCCTCTTCTACTCAAGTCTCTGTAGGCCCAAGCTGACTGTGGGCTCGGAGGCTCTGGA | 1140 | QY | 2233 | GGACAGGCTACGAGGTCATGCCAGCATCATAAACCCCAAGAACACGTACTGTGCTGG | 2292 |
| QY | 1153 | GACCATCTTCTGGGTTCAGGCGCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT | 1212 | Db | 2221 | GGACAGGCTACGAGGTCATGCCAGCATCATAAACCCCAAGAACACGTACTGTGCTGG | 2280 |
| Db | 1141 | GACCATCTTCTGGGTTCAGGCGCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT | 1200 | QY | 2293 | TCGGTATGCCGTGCCAGAGGCCCGCCATGGGCACGTCCGACAGGCCCTTCAAGAGCCA | 2352 |
| QY | 1213 | GCCCCAGCGCTACTTGGCAAAATGGGGCCCTGTCTTCTGTGGAGCTCTTGGGAACACACGCGA | 1272 | Db | 2281 | TCGGTATGCCGTGCCAGAGGCCCGCCATGGGCACGTCCGACAGGCCCTTCAAGAGCCA | 2340 |
| Db | 1201 | GCCCCAGCGCTACTTGGCAAAATGGGGCCCTGTCTTCTGTGGAGCTCTTGGGAACACACGCGCA | 1260 | QY | 2353 | CGTCTCTACTTTGACAGACCTCCAGCCGTACATGGACAGTTCGTGGCTCACTCTCAGGA | 2412 |
| QY | 1273 | GTGGCCCTAGGGGTGCTCTCTAAGAGCACTGCCCGCTCGAGCTGCGGTCAACCCAGC | 1332 | Db | 2341 | CGTCTCTACTTTGACAGACCTCCAGCCGTACATGGACAGTTCGTGGCTCACTCTCAGGA | 2400 |
| Db | 1261 | GTGGCCCTAGGGGTGCTCTCTAAGAGCACTGCCCGCTCGAGCTGCGGTCAACCCAGC | 1320 | QY | 2413 | GACCAGCCGCTGAGGGATGCCGTGTCTATCAGAGACAGTCTCTCTCTGAATGAGGCCAG | 2472 |
| QY | 1333 | AGCGGTGTCTGTGCCGGGAGAGCCCAAGGCTCTGTGGCGGCGCCCGCAGAGAGGA | 1392 | Db | 2401 | GACCAGCCGCTGAGGGATGCCGTGTCTATCAGAGACAGTCTCTCTCTGAATGAGGCCAG | 2460 |
| Db | 1321 | AGCGGTGTCTGTGCCGGGAGAGCCCAAGGCTCTGTGGCGGCGCCCGCAGAGAGGA | 1380 | QY | 2473 | CAGTGGCCCTTCGAGCTCTCTACGCTTATGATGCCACACGCGCTGCGCATCAGGGG | 2532 |
| QY | 1393 | CACAGACCCCGTCGCTGTGTGAGCTGTCTCCGCCAGCAGCAGCGCCCTGGCAGGTGTA | 1452 | Db | 2461 | CAGTGGCCCTTCGAGCTCTCTACGCTTATGATGCCACACGCGCTGCGCATCAGGGG | 2520 |
| Db | 1381 | CACAGACCCCGTCGCTGTGTGAGCTGTCTCCGCCAGCAGCAGCGCCCTGGCAGGTGTA | 1440 | QY | 2533 | CAAGTCTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTCTCTG | 2592 |
| QY | 1453 | CGGCTTCGTGGGGCTGCTCGCGCGGTGGTGGCCCGCAGAGCCTCTGGGGTCCAGGCA | 1512 | Db | 2521 | CAAGTCTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTCTCTG | 2580 |
| Db | 1441 | CGGCTTCGTGGGGCTGCTCGCGCGGTGGTGGCCCGCAGAGCCTCTGGGGTCCAGGCA | 1500 | QY | 2593 | CAGCCTGTCTACGCGGACATGGAGAACAGCTGTTGCGGGGATTCGCGGGAGCGGCT | 2652 |
| QY | 1513 | CAACGAACGCGCTCTCTCAGGAACACCAAGAAGTTCATCTCCCTCGGGAAGCATGCCAA | 1572 | Db | 2581 | CAGCCTGTCTACGCGGACATGGAGAACAGCTGTTGCGGGGATTCGCGGGAGCGGCT | 2640 |
| Db | 1501 | CAACGAACGCGCTCTCTCAGGAACACCAAGAAGTTCATCTCCCTCGGGAAGCATGCCAA | 1560 | QY | 2653 | GCTCTGCTCTTGGTGGATGATTTCTTGTGTGTGACACCTCACTCAACGACGCAAAAC | 2712 |
| QY | 1573 | GCTCTGCTCGAGGAGCTGACGTGGAAGATGACGCTGCGGACTTGGCTGGCGCAG | 1632 | Db | 2641 | GCTCTGCTCTTGGTGGATGATTTCTTGTGTGTGACACCTCACTCAACGACGCAAAAC | 2700 |
| Db | 1561 | GCTCTGCTCGAGGAGCTGACGTGGAAGATGACGCTGCGGACTTGGCTGGCGCAG | 1620 | QY | 2713 | CTTCTCTCAGGACCCCTGGTCCGAGGTGTCCCTCAGTATGCTGTGCTGTGCTGTGCTGTG | 2772 |
| QY | 1633 | GAGCCAGGGTTGGCTGTGTTCCGGCGCAGAGCAGCTGCTGCGTGAGAGATCTGGC | 1692 | Db | 2701 | CTTCTCTCAGGACCCCTGGTCCGAGGTGTCCCTCAGTATGCTGTGCTGTGCTGTGCTGTG | 2760 |
| Db | 1621 | GAGCCAGGGTTGGCTGTGTTCCGGCGCAGAGCAGCTGCTGCTGTGAGAGATCTGGC | 1680 | QY | 2773 | GACAGTGGTGAATTCCTCTGTAGAGACGAGGCCCTGGTGCCACGGCTTTTGTTCAGAT | 2832 |
| QY | 1693 | CAAGTTCTCTGCTGATGAGTGTGTACGTCGAGCTGCTCAGCTCTTCTTTTA | 1752 | Db | 2761 | GACAGTGGTGAATTCCTCTGTAGAGACGAGGCCCTGGTGCCACGGCTTTTGTTCAGAT | 2820 |
| Db | 1681 | CAAGTTCTCTGCTGATGAGTGTGTACGTCGAGCTGCTCAGCTCTTCTTTTA | 1740 | QY | 2833 | GCGCGCCACGCGCTATTCCTCTGTGGGCTGCTGTGGATACCCGAGACCTCGAGGT | 2892 |
| QY | 1753 | TGTCAGGGAGACCACGTTTCAAAAGAACACGCTCTTTTCTTACCGGAAGTGTCTGGAG | 1812 | Db | 2821 | GCGCGCCACGCGCTATTCCTCTGTGGGCTGCTGTGGATACCCGAGACCTCGAGGT | 2880 |
| Db | 1741 | TGTCAGGGAGACCACGTTTCAAAAGAACACGCTCTTTTCTTACCGGAAGTGTCTGGAG | 1800 | QY | 2893 | GCAGAGCGACTACTCCAGCTATSCCGGACCTCCATCAGAGCAGTCTCACTTCAACCG | 2952 |
| QY | 1813 | CAAGTTGCAAGCATTTGGAAATCAGACAGCATTTGAAGAGGGTGCAGCTCGGGAGCTGTC | 1872 | Db | 2881 | GCAGAGCGACTACTCCAGCTATSCCGGACCTCCATCAGAGCAGTCTCACTTCAACCG | 2940 |
| Db | 1801 | CAAGTTGCAAGCATTTGGAAATCAGACAGCATTTGAAGAGGGTGCAGCTCGGGAGCTGTC | 1860 | QY | 2953 | CGGCTTCAAGGCTGGGAGAACATCGCTCGCAAACTCTTTGGGGTCTTTGGGCTGAAGTG | 3012 |
| QY | 1873 | GGAAGCAGAGGTCAGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACCTCCAGACTCCG | 1932 | Db | 2941 | CGGCTTCAAGGCTGGGAGAACATCGCTCGCAAACTCTTTGGGGTCTTTGGGCTGAAGTG | 3000 |
| Db | 1861 | GGAAGCAGAGGTCAGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACCTCCAGACTCCG | 1920 | QY | 3013 | TCACAGCCTGTTTCTGTGGATTTTCAGGTGAACAGCCTCCAGAGGCTGCACCCACATCTA | 3072 |
| QY | 1933 | CTTTCATCCCAAGCCTGACGGGCTGCGGCGGATTTGTGAACATGGACTACGTCTGTGGAGC | 1992 | Db | 3001 | TCACAGCCTGTTTCTGTGGATTTTCAGGTGAACAGCCTCCAGAGGCTGCACCCACATCTA | 3060 |
| Db | 1921 | CTTTCATCCCAAGCCTGACGGGCTGCGGCGGATTTGTGAACATGGACTACGTCTGTGGAGC | 1980 | QY | 3073 | CAAGATCTCTCTGCTGCAGGGCTACAGGTTTCACGCATGTGTGCTGCAGCTCCCCATTTCA | 3132 |

Db 421 CTTGCCCAACAGCGTGACCGACACGACCTGCGGGGAGCGGGGCGTGGGGGCTGTGCTGCG 480
Qy 493 CCGCGTGGGGAGACACGTGCTGGTTCACTGCTGGCACGCTGCGCGCTCTTTTGTGCTGGT 552
Db 481 CCGCGTGGGGAGACACGTGCTGGTTCACTGCTGGCACGCTGCGCGTNTTTGTGCTGGT 540
Qy 553 GCGTCCAGCTGGCGCTACACAGGTGTGCGGGCGCGCGCTGTACACAGCTCGCGCGTGCAC 612
Db 541 GGNTTCCAGCTGGCGCTACCAANGTGTGCGGGCGCGCGCTGTACACAGCTCGCGCGTGCNAC 600
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Db 601 TCAGGCGCGCGCGCGCACACGCTANTGGA - CCGGAANGCGTGTGGGAT - CCAACGCGC 658
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Db 659 CTGGAACCATAGGCTCAGGAGCGCGGGTCCCGCTGGG - CTGCCAGCCCGGGTGGAG 717
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3774 CCCCAGAT 3781
RESULT 13
US-09-438-486-173
; Sequence 173, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..4029
; OTHER INFORMATION: /note= "preliminary sequence for

; OTHER INFORMATION: human TRT cDNA insert of
 ; OTHER INFORMATION: plasmid pGRN121*
 US-09-438-486-173

Query Match 95.3%; Score 3618.6; DB 11; Length 4029;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;

| | | | |
|-----------|----|--|----|
| Oy | 13 | GCAGCGCTGCTCCTGTCGGACGTGGGAAGCCCTGGCCCCCGGCCACCCCCCGATGCC | 72 |
| | | | |
| Dd | 1 | GCAGCGTTCGTCCTGTCGGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCCCGATGCC | 60 |

| | | | |
|----|----|--|-----|
| Qy | 73 | GGCGGCTCCCGCTGCCGAGCGTGCCTCCCTGCTGGCAGCCATACCCGAGGTGCT | 132 |
| Dd | 61 | GGCGCTCCCCGCTGCCGAGCGTGCCTCCCTGCTGGCAGCCATACCCGAGGTGCT | 120 |

| | | | |
|----|-----|---|-----|
| Qy | 133 | GCCGCTGCCACGTTCTGCGGGGCGCTGCGGGCCCCAGGCGCTGCGCGCTGGTGTGTCAGCGCGG | 192 |
| | | | |
| | 121 | GCGCGTGGCCACGTTCTGCGGGGCGCTGCGGGCCCCAGGCGCTGCGCGCTGGCGCGCTGGCGAGCGCGG | 180 |

| | |
|----|-----|
| QY | 252 |
| Db | 240 |

| | | | |
|----|-----|--|-----|
| Qy | 253 | ACGGCCGCCCCCCCGGCGCCCTCTTTCGCCAGGTCTCCTGCCTGAAGGAGCTGGTGCG | 312 |
| | | | |
| Db | 241 | ANGGCNGCCCCCGCGCCGCCCTCTCTTCGCCAGGTGTCTCGCTGAAGNGNCTGGTGCG | 300 |

| | | | |
|----|-----|--|-----|
| Qy | 313 | CCGAGTCTGCAGAGGTGTGGCAGCGCGCGCGAAGCAACGTCTGGCTTCGGCTTCGC | 372 |
| Db | 301 | CCGAGTCTGCANANGTGTGGANCNCGCCGCGGAANAACGTCTGGCTTCGGCTTCGC | 360 |

| Qy | 373 | GCTGCTGGACGGGGCGCGGGGGGCCCCCGAGGCTTCACCAACGCGTGGCGCAGCTA | 432 |
|--|-----|--|-----|
| Dd <th>361</th> <th>GCTGCTGGACGGGGCGCGGGGGGCCCCCGAGGCTTCACCAACGCGTGGCGCAGCTA</th> <th>420</th> | 361 | GCTGCTGGACGGGGCGCGGGGGGCCCCCGAGGCTTCACCAACGCGTGGCGCAGCTA | 420 |

[illegible]

| | QY | 493 | 481 | Db |
|--|-----|-----|-----|----|
| CGCGTGGGCGGACGACGCTGCTTACCTTCTGGCAGCTCGCGCTCTTGTGCTGGT | 552 | | | |
| CGCGTGGGCGGACGACGCTGCTTACCTTCTGGCAGCTCGCGCTCTTGTGCTGGT | | 540 | | |

| | Qy | Db |
|-----|---|-----|
| 553 | GGCTCCAGCTGCGCGCTACCAAGTGTGCGGGCCGCCCTGTACCAAGCTGGCGCTGCAC | 612 |
| 541 | GGNTCCAGCTGCGCGCTACCAAGTGTGCGGGCCGCCCTGTACCAAGCTGGCGCTGCNAC | 600 |

| | QY | Db |
|-----|---|-----|
| 613 | TCAGGGCCGGCCCCCGCCACACGCTACTTGGACCCCGAAGGCGCTCTGGATCGAACGGC | 672 |
| 601 | TCAGGGCCGGCCCCCGCCACACGCTANTGGA-CCCGAAGCGCTCTGGAT-CCAACGGGC | 658 |

| QY | 673 | CTGGAACCATACGCGTCAGGGAGGCCGSGGTC | CGCCCTCGCGCTGCCAGCCCCGGGTGCAG | 732 |
|----|-----|----------------------------------|-------------------------------|-----|
| Dd | 659 | CTGGAACCATACGCGTCAGGGAGGCCGSGGT | CCCCCTGGG-CTGCCAGCCCCGGGTGCAG | 717 |

| QY | 733 | GAGCGCGGGG | CAGTCC | CAGCCG | CACTCT | CGCGTTC | CGCC | CAGAGG | CC | CAGCGT | GGCG | 792 |
|----|-----|--|--------|--------|--------|---------|------|--------|----|--------|------|-----|
| Db | 718 | GAGCGCGGGG <th>CAGTCC</th> <th>CAGCCG</th> <th>CACTCT</th> <th>CGCGTTC</th> <th>CGCC</th> <th>CAGAGG</th> <th>CC</th> <th>CAGCGT</th> <th>GGCG</th> <th>777</th> | CAGTCC | CAGCCG | CACTCT | CGCGTTC | CGCC | CAGAGG | CC | CAGCGT | GGCG | 777 |

| QY | 793 | TGCCCCCTGAGCCGGAGCGGAGCCGCCCTTTGGGCAGGGGTCTCTGGCCCAACCCGGGCAGGAC | 852 |
|--|-----|--|-----|
| Db <th>778</th> <th>TGCCCCCTGAGCCGGAGCGGAGCCGCCCTTTGGGCAGGGGTCTCTGGCCCAACCCGGGCAGGAC</th> <th>837</th> | 778 | TGCCCCCTGAGCCGGAGCGGAGCCGCCCTTTGGGCAGGGGTCTCTGGCCCAACCCGGGCAGGAC | 837 |

| | | | |
|----|-----|---|-----|
| Qy | 853 | GGGTGACCCGAGTGACCGTGGTTTCCTGCTGGTGTACCTGCACAGCCCGCGAAGAC | 912 |
| Db | 838 | GCCTGSACCCGAGTGACCGTGGTTTCCTGCTGGTGTACCTGCACAGCCCGCGAAGAC | 897 |

[illegible]

973 GCACCACGGGGCCCCCATCCACATCGCGGGCCACGACGTCCTGGACACGCGCTGTCC 1032

| | | | |
|----|------|---|------|
| Db | 958 | GCACACGCGGGCCCCCATCCACATCGCGGCCACCAAGT--CCTGGACACAGCCTGTGTC | 1016 |
| Qy | 1033 | CCCCGTTAGCCGAGACCAAGCACTTCCCTCTACTCTCTCAGGGGACAAAGACAGCAGTGGC | 1092 |
| Db | 1017 | CCCCGTTAGCCGAGACCAAGCACTTCCCTCTACTCTCTCAGGGGACAAAGNA--CACTGGC | 1074 |
| Qy | 1093 | GCCCTCCTTCTACTC-AGCTCTCTGAGGGCCAGCCTCTACTGCGCTCGGAGGCTCGTGG | 1151 |
| Db | 1075 | NCCCTCCTCTACTCAATATATCTGAGGCCAGGCTGACTGGCTTCGGGAGGTTCTGGT | 1134 |
| Qy | 1152 | AGACCATTTTCTGGGTTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGGCC | 1211 |
| Db | 1135 | GAGACANTCTTCTGGTTTCCAGGCTTGGATGCCA-GGATTCGCGCAGGTTGCCCGGCC | 1193 |
| Qy | 1212 | TGCCCCAGCGCTACTGTGCAAAATGGGCCCTGTTTCTGGAGCTGTCTGGGAACACAGCGC | 1271 |
| Db | 1194 | TGCCCCAGGNTACTGTCAAAATGGGCCCTGTTTCTGGAGCTGTCTGGGAACACAGCGC | 1253 |
| Qy | 1272 | AGTGCCCTTACGGGGTGCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTACACCCAG | 1331 |
| Db | 1254 | AGTGCCCTTACGGGGTTCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTACACCCAG | 1313 |
| Qy | 1332 | CAGCGGTGTCTGTGCCCCGGAGAGGCCCAAGGCTCTGTGGGCCCCCGAGAGGAGG | 1391 |
| Db | 1314 | CAGCGGTGTCTGTGCCCCGGAGAGGCCCAAGGCTCTGTGGGCCCCCGAGAGGAGG | 1373 |
| Qy | 1392 | -ACACAGACCCCGTCCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTG | 1450 |
| Db | 1374 | AACACAGACCCCGTCCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTG | 1433 |
| Qy | 1451 | TACGGCTTCGTGCGGGCTCGCTCGCGCGCTGCTGCCCCAGGCTCTGGGCTCCAGG | 1510 |
| Db | 1434 | TACGGCTTCGTGCGGGCTGCCCTGGCGCGCTGCTGCCCCAGGCTCTGGGCTCCAGG | 1493 |
| Qy | 1511 | CACAACGAACCGCGCTTCTCAGGAACACCAAGAAGTTCAATCTCTGGGGAAGCATGCC | 1570 |
| Db | 1494 | CACAACGAACCGCGCTTCTCAGGAACACCAAGAAGTTCAATCTCTGGGGAAGCATGCC | 1553 |
| Qy | 1571 | AAGCTCTCGCTCAGGAGCTGAGCTGGAAGTGAAGTGGGAGCTGCGGACTGCGCTTGGCTGCC | 1630 |
| Db | 1554 | AAGCTCTCGCTCAGGAGCTGAGCTGGAAGTGAAGTGGGAGCTGCGGACTGCGCTTGGCTGCC | 1613 |
| Qy | 1631 | AGGAGCCAGGGTTGGCTGTGTCCGGCCGACAGCACCGCTGCGTGAGGAGATCCTG | 1690 |
| Db | 1614 | AGGAGCCAGGGTTGGCTGTGTTCGGCCGACAGCACCGCTGCGTGAGGAGATCCTG | 1673 |
| Qy | 1691 | GCCAACTTCTGACACTGGCTGATGAGTGTGATGCTGCGAGCTGCTCAGGCTCTTCTTT | 1750 |
| Db | 1674 | GCCAACTTCTGCACTGGCTGATGAGTGTGATGCTGCGAGCTGCTCAGGCTCTTCTTT | 1733 |
| Qy | 1751 | TATGTACGGAGACACAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGG | 1810 |
| Db | 1734 | TATGTACGGAGACACAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGG | 1793 |
| Qy | 1811 | AGCAAGTTGCAAGCATTGGAATCAGACAGCACTTGAAGAGGCTGACGCTGCCGGAGCTG | 1870 |
| Db | 1794 | AGCAAGTTGCAAGCATTGGAATCAGACAGCACTTGAAGAGGCTGACGCTGCCGGAGCTG | 1853 |
| Qy | 1871 | TCGGAAGCAGGTTACGGCAGCATTCGGGAAGCAGGCCCTGCTGAGCTGCCAGCTC | 1930 |
| Db | 1854 | TCGGAAGCAGGTTACGGCAGCATTCGGGAAGCAGGCCCTGCTGAGCTGCCAGCTC | 1913 |
| Qy | 1931 | CGCTTCATCCCCAAGCTGACGGGCTCGGCCCATTTGTGAACATGACATACGTCGTGGGA | 1990 |
| Db | 1914 | CGCTTCATCCCCAAGCTGACGGGCTCGGCCCATTTGTGAACATGACATACGTCGTGGGA | 1973 |
| Qy | 1991 | GCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTTCAGGGTTGAAGGACATG | 2050 |
| Db | 1974 | GCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTTCAGGGTTGAAGGACATG | 2033 |
| Qy | 2051 | TTCAGCGTGTCAACTACGAGCGGCGCGGCCCGCCGCTCTCTGGGCGCTCTGTGCTG | 2110 |

| | | | |
|------|----|---|------|
| 2034 | Db | TTCCAGCGTGTCTAACTACGAGCGGGCGGGCGCCCGGCGCTCTCTGGGGCGCTCTGTGTGCTG | 2099 |
| 2111 | Qy | GGCCTGGACGATATCCACAGGGCGCTCGCGCACCTTCGTGTCTGTGTGGGGGCCACAGGAC | 2170 |
| | | | 2171 |
| | | GGCCTGGACGATATCCACAGGGCGCTGGCGCACCTTCGTGTGTGTGTGGGGGCCACAGGAC | 2153 |
| 2171 | Qy | CCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCG | 2230 |
| | | | 2231 |
| | | CCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCG | 2213 |
| 2231 | Qy | CAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCGACAGAACAGTACTCGGTG | 2290 |
| | | | 2291 |
| | | CAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCGACAGAACAGTACTCGGTG | 2273 |
| 2291 | Qy | CGTCGCTATGCCGTGTCCAGAAAGCGCGCCATGGCAGCTCCGCAAGGCGTTCAAGAGC | 2350 |
| | | | 2351 |
| | | CGTCGCTATGCCGTGTCCAGAAAGCGCGCCATGGCAGCTCCGCAAGGCGTTCAAGAGC | 2333 |
| 2351 | Qy | CAGCTCTCTACCTTGACAGACCTTCAGCGGTACATCGGACAGTTCGTGGCTCACCTGCAG | 2410 |
| | | | 2411 |
| | | CAGCTCTCTACCTTGACAGACCTTCAGCGGTACATCGGACAGTTCGTGGCTCACCTGCAG | 2393 |
| 2411 | Qy | GAGCACCAGCCGCTGAGGATGCCCTGTCATCGACGAGAGCTTCCTCGAATGAGGCC | 2470 |
| | | | 2471 |
| | | GAGCACCAGCCGCTGAGGATGCCCTGTCATCGACGAGAGCTTCCTCGAATGAGGCC | 2453 |
| 2471 | Qy | AGCAGTGGCGCTTCGACGCTTCCTCACGCTTCATGTGCCACACCGCTGGCGCATCAGS | 2530 |
| | | | 2531 |
| | | AGCAGTGGCGCTTCGACGCTTCCTCACGCTTCATGTGCCACACCGCTGGCGCATCAGS | 2513 |
| 2531 | Qy | GGCAAGTCTCAGTCCAGTCCGAGGGGATCCCGCAGGGCTCCTCTCTCCAGCGTGCCTC | 2590 |
| | | | 2591 |
| | | GGCAAGTCTCAGTCCGAGGGGATCCCGCAGGGCTCCTCTCTCCAGCGTGCCTC | 2573 |
| 2591 | Qy | TGCAGCGCTGTGCTACGGCGACATGGAGAACAGACTGTTTGCGGGGATTCGGCGGGACGGG | 2650 |
| | | | 2651 |
| | | TGCAGCGCTGTGCTACGGCGACATGGAGAACAGACTGTTTGCGGGGATTCGGCGGGACGGG | 2633 |
| 2651 | Qy | CTGCTCCTGGCTTTGGTGATTTCTTGTGGTGACACCTCACCTCACCCACGCGGAAA | 2710 |
| | | | 2711 |
| | | CTGCTCCTGGCTTTGGTGATTTCTTGTGGTGACACCTCACCTCACCCACGCGGAAA | 2693 |
| 2711 | Qy | ACCTTCTCAGGACCGTGTCCGAGGTGCCCTTGAGTATGGCTGCGTGTGTAACCTTGGCGG | 2770 |
| | | | 2771 |
| | | ACCTTCTCAGGACCGTGTCCGAGGTGCCCTTGAGTATGGCTGCGTGTGTAACCTTGGCGG | 2753 |
| 2771 | Qy | AAGCAGTGGTGAACTTCCCTGTAGAGAGAGCGCCCTGGTGGCAGCGCTTTGTTCAG | 2830 |
| | | | 2831 |
| | | AAGCAGTGGTGAACTTCCCTGTAGAGAGAGCGCCCTGGTGGCAGCGCTTTGTTCAG | 2813 |
| 2831 | Qy | ATCGCGGCCACAGCGCTATTCCCTGGTGGGGCGCTGCTGTGTGATACCGGAGCCCTGGAG | 2890 |
| | | | 2891 |
| | | ATCGCGGCCACAGCGCTATTCCCTGGTGGGGCGCTGCTGTGTGATACCGGAGCCCTGGAG | 2873 |
| 2891 | Qy | GTCCAGAGCGACTTCTCCAGCTATGCCCGGACCTCCATCAGAGCCAGCTTCACCTTCAAC | 2950 |
| | | | 2951 |
| | | GTCCAGAGCGACTTCTCCAGCTATGCCCGGACCTCCATCAGAGCCAGCTTCACCTTCAAC | 2933 |
| 2951 | Qy | CGCGGCTTCAAGGCTGGGAGGAACATCGCTCGCAAACTCTTTGGGTCTTTGGCGCTGAAG | 3010 |
| | | | 3011 |
| | | CGCGGCTTCAAGGCTGGGAGGAACATCGCTCGCAAACTCTTTGGGTCTTTGGCGCTGAAG | 2993 |
| 3011 | Qy | TGTCACAGCGCTGTTCTTGATTTGCAAGTGAACAGCGCTCCAGACGGTGTGCACCAACATC | 3070 |
| | | | 3071 |
| | | TGTCACAGCGCTGTTCTTGATTTGCAAGTGAACAGCGCTCCAGACGGTGTGCACCAACATC | 3053 |
| 3071 | Qy | TACAAGATCCTCTGTGTGACGGCGTACAGGTTTTCACGCGATGTGTGTGACAGCTCCCATTT | 3130 |
| | | | 3131 |
| | | TACAAGATCCTCTGTGTGACGGCGTACAGGTTTTCACGCGATGTGTGTGACAGCTCCCATTT | 3113 |
| 3131 | Qy | CATCAGCAAGTTTGGAGAACCCACCATTTTTTCTGGGGGTCACTCTGACAGCGGCTCC | 3190 |
| | | | 3191 |
| | | CATCAGCAAGTTTGGAGAACCCACCATTTTTTCTGGGGGTCACTCTGACAGCGGCTCC | 3173 |

| | | | |
|----|------|---|------|
| Qy | 3191 | CTCTGCTACTCCATCTCTGAAAGCCCAAGACGCAGGAGTGTGCTGGGGGGCCAAAGGGCGCC | 3250 |
| | | | |
| Db | 3174 | CTCTGCTACTTCCATCTCTGAAAGCCCAAGACGCAGGAGTGTGCTGGGGGGCCAAAGGGCGCC | 3233 |
| | | | |
| Qy | 3251 | GCGGGCCCTCTGCCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAACATTCCTTGCCTCAAG | 3310 |
| Db | 3234 | GCGGGCCCTCTGCCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAACATTCCTTGCCTCAAG | 3293 |
| | | | |
| Qy | 3311 | CTGACTGGACACCGTGTACCTACGTGCCACTCCTTGGGTCTACTCAGCAGACGCCACAGCG | 3370 |
| Db | 3294 | CTGACTCGACACCGTGTACCTACGTGCCACTCCTTGGGTCTACTCAGCAGACGCCACAGCG | 3353 |
| | | | |
| Qy | 3371 | CAGCTGAGTCGGAGCTCCCGGGAGACGCTGACTGCCCTGGAGGCCGAGCCCAACCCG | 3430 |
| Db | 3354 | CAGCTGAGTCGGAGCTCCCGGGAGACGCTGACTGCCCTGGAGGCCGAGCCCAACCCG | 3413 |
| | | | |
| Qy | 3431 | GCACTGCCCTCAGACTTCAAGACCATCCTTGGACTGATGGCCACCCGCCACAGCCAGGCC | 3490 |
| Db | 3414 | GCACTGCCCTCAGACTTCAAGACCATCCTTGGACTGATGGCCACCCGCCACAGCCAGGCC | 3473 |
| | | | |
| Qy | 3491 | GAGAGCAGACACAGAGCCCTGTACGCCGGGGCTCTAGTCCAGGGAGGGAGGGGGCG | 3550 |
| Db | 3474 | GAGAGCAGACACAGAGCCCTGTACGCCGGGGCTCTAGTCCAGGGAGGGAGGGGGCG | 3533 |
| | | | |
| Qy | 3551 | CCACACCCAGGCCCGCACCGCTGGAGTCTGAGGCCCTGAGTGAGTGTGTCGGCCGAGGCC | 3610 |
| Db | 3534 | CCACACCCAGGCCCGCACCGCTGGAGTCTGAGGCCCTGAGTGAGTGTGTCGGCCGAGGCC | 3593 |
| | | | |
| Qy | 3611 | TGCATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCCAAGG | 3670 |
| Db | 3594 | TGCATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCCAAGG | 3653 |
| | | | |
| Qy | 3671 | CTGAGTGTCCAGCACACCTCGCCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCACCC | 3730 |
| Db | 3654 | CTGAGTGTCCAGCACACCTCGCCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCACCC | 3713 |
| | | | |
| Qy | 3731 | CAGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT | 3790 |
| Db | 3714 | CAGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT | 3773 |
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| Qy | 3791 | CCCTGTAT | 3798 |
| Db | 3774 | CCCCAGAT | 3781 |

RESULT 14

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US-10-053-758-173
; Sequence 173, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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| 1 | APPLICATION NUMBER: US/10/053,758 | 493 | CCGCTGGGCGACGACGCTGCTGTTTACCTGTGGCAGCTGCGCGCTCTTTTGTCTGCT 555 |
| 2 | FILING DATE: 18-Jan-2002 | 481 | |
| 3 | CLASSIFICATION: 536 | 481 | CCGCTGGGCGACGACGCTGCTGTTTACCTGTGGCAGCTGCGCGGNTTTTGTGCTGCT 540 |
| 4 | PRIOR APPLICATION DATA: | | |
| 5 | APPLICATION NUMBER: US/08/854,050 | 553 | GGTCTCCAGCTGCGCCTACAGGTGTGCGGGCGCGGCTGTACAGCTGCGGCTGCGCAC 612 |
| 6 | FILING DATE: 09-MAY-1997 | | |
| 7 | APPLICATION NUMBER: US/08/851,843 | | |
| 8 | FILING DATE: 06-MAY-1997 | 541 | GGNTCCAGCTGCGCCTAGCANGTGTGCGGGCGCGCTGTACACAGCTGCGGCTGCGCAC 600 |
| 9 | APPLICATION NUMBER: US/08/846,017 | 613 | TCAGGCG 672 |
| 10 | FILING DATE: 25-APR-1997 | | |
| 11 | APPLICATION NUMBER: US/08/844,419 | 601 | TCAGGCG 658 |
| 12 | FILING DATE: 18-APR-1997 | 673 | CTGGAACCATAGCGTTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 732 |
| 13 | APPLICATION NUMBER: US/08/724,643 | 659 | CTGGAACCATAGCGTTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 717 |
| 14 | FILING DATE: 01-OCT-1996 | | |
| 15 | ATTORNEY/AGENT INFORMATION: | | |
| 16 | NAME: Apple, Randolph T. | 733 | GAGCGCGGGGCGAGTGCAGCGCGAGTCTGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 792 |
| 17 | REGISTRATION NUMBER: 36,429 | | |
| 18 | REFERENCE/DOCKET NUMBER: 015389-0029300US | 718 | GAGCGCGGGGCGAGTGCAGCGCGAGTCTGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 777 |
| 19 | TELECOMMUNICATION INFORMATION: | | |
| 20 | TELEPHONE: (415) 576-0200 | 793 | TGCGCGCTGAGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 852 |
| 21 | TELEFAX: (415) 576-0300 | | |
| 22 | INFORMATION FOR SEQ ID NO: 173: | 778 | TGCGCGCTGAGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 837 |
| 23 | SEQUENCE CHARACTERISTICS: | | |
| 24 | LENGTH: 4029 base pairs | 853 | GCCTGACCGAGTACCGTGGTTCCTGCTGTGTGTGTCTACCTGTGCTGTGTGTGTGTGTGTGT 912 |
| 25 | TYPE: nucleic acid | | |
| 26 | STRANDEDNESS: single | 838 | GCCTGACCGAGTACCGTGGTTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897 |
| 27 | TOPOLOGY: linear | | |
| 28 | MOLECULE TYPE: cDNA | 913 | CACCTCTTTGGAGGGTGCCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 972 |
| 29 | FEATURE: | | |
| 30 | NAME/KEY: | 898 | CACCTCTTTGGAGGGTGCCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 957 |
| 31 | LOCATION: 1..4029 | | |
| 32 | OTHER INFORMATION: /note= "preliminary sequence for | 973 | GCACACG 1032 |
| 33 | human TRT cDNA insert of | | |
| 34 | Plasmid pGRN121" | 958 | GCACACG 1016 |
| 35 | SEQUENCE DESCRIPTION: SEQ ID NO: 173: | | |
| 36 | US-10-053-758-173 | 1033 | CCGCGTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1092 |
| 37 | | | |
| 38 | Query Match | 1017 | CCGCGTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1074 |
| 39 | Best Local Similarity | | |
| 40 | Matches 3725; Conservative | 1093 | GCGCT 1151 |
| 41 | | | |
| 42 | | 1075 | NCCT 1134 |
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| 44 | | 1152 | AGACCACTTTTCTGGGTTCACGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGG 1211 |
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| 47 | | | |
| 48 | | 1212 | TGCGCGCGCT 1271 |
| 49 | | | |
| 50 | | 1194 | TGCGCGCGCT 1253 |
| 51 | | | |
| 52 | | 1272 | AGTGCCTCTACGCGGCT 1331 |
| 53 | | | |
| 54 | | 1254 | AGTGCCTCTACGCGGCT 1313 |
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| 56 | | 1332 | CAGCGGCT 1391 |
| 57 | | | |
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| 60 | | 1392 | -ACACAGACCCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1450 |
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| 62 | | 1374 | AACACAGACCCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1433 |
| 63 | | | |
| 64 | | 1451 | TACGGGTTCTGCGGGGCT 1510 |
| 65 | | | |
| 66 | | 1434 | TACGGGTTCTGCGGGGCT 1493 |
| 67 | | | |
| 68 | | 1511 | CACACGACCGCGCT 1570 |
| 69 | | | |
| 70 | | 1494 | CACACGACCGCGCT 1553 |
| 71 | | | |
| 72 | | 1571 | AAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGAGTGCAGGAGTGCAGGAGTGC 1630 |

[illegible]

| | | | |
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| Db | 2634 | CTGCTCTCTCGGCTTTGGTGGAATGATTTCTTGTTGGTGACACCTCACCTTCACCCACGGCGAAA | 2659 |
| QY | 2711 | ACCTTCTCTCAGAACCCCTGGTCCGAGGTGTCCTCTGAGTATGGCTGCGGTGGTGAACCTTGGCGG | 2770 |
| Db | 2694 | ACCTTCTCTCAGAACCCCTGGTCCGAGGTGTCCTCTGAGTATGGCTGCGGTGGTGAACCTTGGCGG | 2753 |
| QY | 2771 | AAGCAGTGGTGAACTTCCCTGTGTAAGACGAGGCCCTGGGTGGCAGCGCTTTGTTGTCAG | 2830 |
| Db | 2754 | AAGCAGTGGTGAACTTCCCTGTGTAAGACGAGGCCCTGGGTGGCAGCGCTTTGTTGTCAG | 2813 |
| QY | 2831 | ATGCGGGCCACAGCGCTATTCCCTGTGTGGGCTGCTGCTGCATACCCGGACCCCTGGAG | 2890 |
| Db | 2814 | ATGCGGGCCACAGCGCTATTCCCTGTGTGGGCTGCTGCTGCATACCCGGACCCCTGGAG | 2873 |
| QY | 2891 | GTGCAGAGCGACTACTCCAGCTATGCCGCCGACCTCCATCAGAGCCAGTCTCAGCTTCAAC | 2950 |
| Db | 2874 | GTGCAGAGCGACTACTCCAGCTATGCCGCCGACCTCCATCAGAGCCAGTCTCAGCTTCAAC | 2933 |
| QY | 2951 | CGCGGCTTCAAGGCTGGGAGAACATCGCTGCGAAACTCTTTGGGCTTTGCGGCTGAAG | 3010 |
| Db | 2934 | CGCGGCTTCAAGGCTGGGAGAACATCGCTGCGAAACTCTTTGGGCTTTGCGGCTGAAG | 2993 |
| QY | 3011 | TGTCACAGCCGTTCTTGGATTTCAGAGTGAACAGCGCTCCAGAGGTGTGCACCAACATC | 3070 |
| Db | 2994 | TGTCACAGCCGTTCTTGGATTTCAGAGTGAACAGCGCTCCAGAGGTGTGCACCAACATC | 3053 |
| QY | 3071 | TACAAGATCTCTCCGCTGACAGGCGTACAGGTTTTCACGCATGTGTGCTGACAGCTCCCATTT | 3130 |
| Db | 3054 | TACAAGATCTCTCCGCTGACAGGCGTACAGGTTTTCACGCATGTGTGCTGACAGCTCCCATTT | 3113 |
| QY | 3131 | CATCAGCAAGTTTGGAAAGAACCCACATTTTCTGCGCTCATCTCTGACACGGGCTCC | 3190 |
| Db | 3114 | CATCAGCAAGTTTGGAAAGAACCCACATTTTCTGCGCTCATCTCTGACACGGGCTCC | 3173 |
| QY | 3191 | CTCTGCTACTCCATCTTGAAGCAAGCAAGCGCAGGGATGTCGTGGGGGCCAAGGGCGCC | 3250 |
| Db | 3174 | CTCTGCTACTCCATCTTGAAGCAAGCAAGCGCAGGGATGTCGTGGGGGCCAAGGGCGCC | 3233 |
| QY | 3251 | GCCGGCCCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAG | 3310 |
| Db | 3234 | GCCGGCCCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAG | 3293 |
| QY | 3311 | CTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCCAGCG | 3370 |
| Db | 3294 | CTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCCAGCG | 3353 |
| QY | 3371 | CAGCTGAGTCGGAAGCTCCCGGGGACACCGTGCCTGAGGCCCTGAGGCCCGCAGCCACCCG | 3430 |
| Db | 3354 | CAGCTGAGTCGGAAGCTCCCGGGGACACCGTGCCTGAGGCCCTGAGGCCCGCAGCCACCCG | 3413 |
| QY | 3431 | GCATGCCCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCGGCCACAGCCAGGCC | 3490 |
| Db | 3414 | GCATGCCCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCGGCCACAGCCAGGCC | 3473 |
| QY | 3491 | GAGAGCAGACACAGCAGCCCTGTACCGCGGGCTCTACCTCCAGGGAGGGAGGGCGG | 3550 |
| Db | 3474 | GAGAGCAGACACAGCAGCCCTGTACCGCGGGCTCTACCTCCAGGGAGGGAGGGCGG | 3533 |
| QY | 3551 | CCCACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAGTCTTTGGCCGAGGCC | 3610 |
| Db | 3534 | CCCACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAGTCTTTGGCCGAGGCC | 3593 |
| QY | 3611 | TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGG | 3670 |
| Db | 3594 | TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGG | 3653 |
| QY | 3671 | CTGAGTGTCCAGCACACTCGCGCTTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCC | 3730 |
| Db | 3654 | CTGAGTGTCCAGCACACTCGCGCTTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCC | 3713 |
| QY | 3731 | CAGGGCCAGCTTTTCTCACAGAGGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT | 3790 |
| Db | 3714 | CAGGGCCAGCTTTTCTCACAGAGGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT | 3773 |

| | | | |
|----|------|--|------|
| Db | 1075 | NCCCTCCTTCTTACATCAATATATCTGAGGCCAGCCCTGACTGGCGTTCCGGAGGTTCTGTG | 1134 |
| QY | 1152 | AGACCATCTTTCTGGTTCAGGCCCTTGATGCGCAGGGACTCCCCGACAGTTGCCCCGCC | 1211 |
| Db | 1135 | GAGACATCTTTCTGGTTCAGGCCCTTGATGCCA-GGATTCGCCGACAGTTGCCCCGCC | 1193 |
| QY | 1212 | TGCCCCAGGCTTACTTGGCAAAATCGGCCCTCTTTCTGTGAGCTGCTTGGGAACCAAGCGC | 1271 |
| Db | 1194 | TGCCCCAGGCTTACTTGGCAAAATCGGCCCTCTTTCTGTGAGCTGCTTGGGAACCAAGCGC | 1253 |
| QY | 1272 | AGTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGGAGCTGCGGTCACCCCCAG | 1331 |
| Db | 1254 | AGTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGGAGCTGCGGTCACCCCCAG | 1313 |
| QY | 1332 | CAGCCGGTCTGTGCCCCGGGAGAACCCAGGGCTCTGTGCGGCCCCCGCAGGAGG | 1391 |
| Db | 1314 | CAGCCGGTCTGTGCCCCGGGAGAACCCAGGGCTCTGTGCGGCCCCCGCAGGAGG | 1373 |
| QY | 1392 | -ACACAGACCCCGCTGCTGTGAGCTGTCTCCGCCAGCACAGACGCCCTGGCAGGTG | 1450 |
| Db | 1374 | ACACAGACCCCGCTGCTGTGAGCTGTCTCCGCCAGCACAGACGCCCTGGCAGGTG | 1433 |
| QY | 1451 | TACGGCTCTGTGCGGGCTGCTGTGCGCGGCTGTGTCGCCCAAGGCTCTGGGGCTCCAGG | 1510 |
| Db | 1434 | TACGGCTCTGTGCGGGCTGCTGTGCGCGGCTGTGTCGCCCAAGGCTCTGGGGCTCCAGG | 1493 |
| QY | 1511 | CACACGAGCGCGCTCTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAGCATGCC | 1570 |
| Db | 1494 | CACACGAGCGCGCTCTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAGCATGCC | 1553 |
| QY | 1571 | AAGCTCTCGCTCAGGAGCTGACGTGGAGATGAGCGTCGGGACTGCGCTGGCTGGCG | 1630 |
| Db | 1554 | AAGCTCTCGCTCAGGAGCTGACGTGGAGATGAGCGTCGGGACTGCGCTGGCTGGCG | 1613 |
| QY | 1631 | AGGAGCCCAAGGGTTGGCTGTCTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCCTG | 1690 |
| Db | 1614 | AGGAGCCCAAGGGTTGGCTGTCTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCCTG | 1673 |
| QY | 1691 | GCCAGTCTCTGCAGTGGCTGATGATGTGTGATGTGATGTGATGTGATGTGATGTGATGTG | 1750 |
| Db | 1674 | GCCAGTCTCTGCAGTGGCTGATGATGTGTGATGTGATGTGATGTGATGTGATGTGATGTG | 1733 |
| QY | 1751 | TATGTACAGGACACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG | 1810 |
| Db | 1734 | TATGTACAGGACACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG | 1793 |
| QY | 1811 | AGCAAGTTCGAAGCATTGGAAATCAGACAGCACTTGAAGAGGCTGAGCTGCGGGAGCTG | 1870 |
| Db | 1794 | AGCAAGTTCGAAGCATTGGAAATCAGACAGCACTTGAAGAGGCTGAGCTGCGGGAGCTG | 1853 |
| QY | 1871 | TGGGAAGCAGAGGTACAGGAGCATCGGGAAGCCAGGCCCGCTGTGATGATGATGATGATG | 1930 |
| Db | 1854 | TGGGAAGCAGAGGTACAGGAGCATCGGGAAGCCAGGCCCGCTGTGATGATGATGATGATG | 1913 |
| QY | 1931 | CGCTTCATCCCAAGCTGACGGCTGCGGGCGATGTGAACATGAGCTACCTCGTGGGA | 1990 |
| Db | 1914 | CGCTTCATCCCAAGCTGACGGCTGCGGGCGATGTGAACATGAGCTACCTCGTGGGA | 1973 |
| QY | 1991 | GCCAGAACGTTCCGAGAGAAAAGAGGCGGAGCGCTCTCACCTCGAGGCTGAAGGCACTG | 2050 |
| Db | 1974 | GCCAGAACGTTCCGAGAGAAAAGAGGCGGAGCGCTCTCACCTCGAGGCTGAAGGCACTG | 2033 |
| QY | 2051 | TTACAGGCTCTCAACTACGAGCGGGCGGCCCGGCCCTCTGCGGCCCTCTGTGCTG | 2110 |
| Db | 2034 | TTACAGGCTCTCAACTACGAGCGGGCGGCCCGGCCCTCTGCGGCCCTCTGTGCTG | 2093 |
| QY | 2111 | GCCCTGGAGCATATCCACAGGCGCTGGGCCACTTTCGTGCTGCTGCTGCTGCTGCTGCTG | 2170 |
| Db | 2094 | GCCCTGGAGCATATCCACAGGCGCTGGGCCACTTTCGTGCTGCTGCTGCTGCTGCTGCTG | 2153 |
| QY | 2171 | CGCGGCCCTGTGCTTCTCAAGGTGGATGTGACGGCGCGCTGACACACCATCCCTC | 2230 |
| Db | 2154 | CGCGGCCCTGTGCTTCTCAAGGTGGATGTGACGGCGCGCTGACACACCATCCCTC | 2213 |
| QY | 2231 | CAGGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACAGCTACTCGGTG | 2290 |
| Db | 2214 | CAGGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACAGCTACTCGGTG | 2273 |
| QY | 2291 | CGTCGGTATGCGGTGCTCAGAGGCGCCCATGCGCAGCTCGCGAAGGCTTCAAGAGC | 2350 |
| Db | 2274 | CGTCGGTATGCGGTGCTCAGAGGCGCCCATGCGCAGCTCGCGAAGGCTTCAAGAGC | 2333 |
| QY | 2351 | CACGTCTTACCTTGACAGACCTTCCAGCCGTACATCGACAGTTCGTGGCTCACCTGCAG | 2410 |
| Db | 2334 | CACGTCTTACCTTGACAGACCTTCCAGCCGTACATCGACAGTTCGTGGCTCACCTGCAG | 2393 |
| QY | 2411 | GAGACAGCCCGCTGAGGGATGCCGTCTCATCGACAGCAGCTCTCCCTGATGAGGCC | 2470 |
| Db | 2394 | GANAACAGCCCGCTGAGGGATGCCGTCTCATCGACAGCAGCTCTCCCTGATGAGGCC | 2453 |
| QY | 2471 | AGCAGTGGCTCTTTCACGCTTCTTACGCTTTCATGCGTTCATGCGCACCCGCTGCCATCAGG | 2530 |
| Db | 2454 | AGCAGTGGCTCTTTCACGCTTCTTTCATGCGTTCATGCGCACCCGCTGCCATCAGG | 2513 |
| QY | 2531 | GGCAAGTCTACGTCCAGTGCCAGGGGATCCCGAGGGCTCCATCTCTCCAGCTGCTC | 2590 |
| Db | 2514 | GGCAAGTCTACGTCCAGTGCCAGGGGATCCCGAGGGCTCCATCTCTCCAGCTGCTC | 2573 |
| QY | 2591 | TGCAGCCTGTGCTACGGCCACATGGAGAACAGCTGTTTGGGGGATTCGGCGGGAGCGG | 2650 |
| Db | 2574 | TGCAGCCTGTGCTACGGCCACATGGAGAACAGCTGTTTGGGGGATTCGGCGGGAGCGG | 2633 |
| QY | 2651 | CTGCTCTCGCTTGTGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACCGGAA | 2710 |
| Db | 2634 | CTGCTCTCGCTTGTGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACCGGAA | 2693 |
| QY | 2711 | ACCTTCTCAGGACCCCTGCTCGAGGTGCTCCCTGAGTATGGCTGCTGCTGCTGCTGCTG | 2770 |
| Db | 2694 | ACCTTCTCAGGACCCCTGCTCGAGGTGCTCCCTGAGTATGGCTGCTGCTGCTGCTGCTG | 2753 |
| QY | 2771 | AGACAGTGTGTAACCTTCCCTGTAGAGAGGAGGCCCTGGTGGGACGGCTTTGTTCAG | 2830 |
| Db | 2754 | AGACAGTGTGTAACCTTCCCTGTAGAGAGGAGGCCCTGGTGGGACGGCTTTGTTCAG | 2813 |
| QY | 2831 | ATGCGGGCCACGCGCTTATTCCTGCTGCGGCTGCTGCTGATACCGGACCCCTGGAG | 2890 |
| Db | 2814 | ATGCGGGCCACGCGCTTATTCCTGCTGCGGCTGCTGCTGATACCGGACCCCTGGAG | 2873 |
| QY | 2891 | GTGACAGGACTACTCCAGCTATGCCGGAACCTCCATCAGAGCCAGTCTCACCTTCAAC | 2950 |
| Db | 2874 | GTGACAGGACTACTCCAGCTATGCCGGAACCTCCATCAGAGCCAGTCTCACCTTCAAC | 2933 |
| QY | 2951 | CGGGGTTCAAGGCTGGGAGAACATGCGTCCGAAACTCTTTGGGGTCTTTGGGGCTGAAG | 3010 |
| Db | 2934 | CGGGGTTCAAGGCTGGGAGAACATGCGTCCGAAACTCTTTGGGGTCTTTGGGGCTGAAG | 2993 |
| QY | 3011 | TGTCACAGCTGTTCCTGATTTGCAAGGTGAACAGCTCCAGACGCTGTCACCAACATC | 3070 |
| Db | 2994 | TGTCACAGCTGTTCCTGATTTGCAAGGTGAACAGCTCCAGACGCTGTCACCAACATC | 3053 |
| QY | 3071 | TACAAGTCTCTGCTGAGGCTTACAGCTTTACGCTATGTGCTGCTGCTGCTGCTGCTGCTG | 3130 |
| Db | 3054 | TACAAGTCTCTGCTGAGGCTTACAGCTTTACGCTATGTGCTGCTGCTGCTGCTGCTGCTG | 3113 |
| QY | 3131 | CATCAGAAAGTTGGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGCTGCTC | 3190 |
| Db | 3114 | CATCAGAAAGTTGGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGCTGCTC | 3173 |
| QY | 3191 | CTCTGCTACTTCCATCTGAAAGAACAGGAGGATGCTGCTGGGGGCAAGGGGCC | 3250 |
| Db | 3174 | CTCTGCTACTTCCATCTGAAAGAACAGGAGGATGCTGCTGGGGGCAAGGGGCC | 3233 |
| QY | 3251 | GCGGGCCCTCTGCGCTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 3310 |
| Db | 3234 | GCGGGCCCTCTGCGCTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 3293 |

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QY 3311 CTGACTCGACACCGGTGTACCTAGCTAGTGCCTCTCTGGGGTCACTCAGGACAGCCAGAGC 3370
Db |||||||
QY 3294 CTGACTCGACACCGGTGTACCTAGCTAGTGCCTCTCTGGGGTCACTCAGGACAGCCAGAGC 3353
Db |||||||
QY 3371 CAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCGCAGCCAAACCG 3430
Db |||||||
QY 3354 CAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCGCAGCCAAACCG 3413
Db |||||||
QY 3431 GCATGCCCCCTAGACTTCAAGACCATCTGACTGATGSCCATCCCGCCACAGCCAGGCC 3490
Db |||||||
QY 3414 GCATGCCCCCTAGACTTCAAGACCATCTGACTGATGSCCATCCCGCCACAGCCAGGCC 3473
Db |||||||
QY 3491 GAGAGCAGACACCGACGACCCCTGTACGCCCGGGCTCTACGTCCAGGAGGAGGGGGCG 3550
Db |||||||
QY 3474 GAGAGCAGACACCGACGACCCCTGTACGCCCGGGCTCTACGTCCAGGAGGAGGGGGCG 3533
Db |||||||
QY 3551 CCCACACCGAGCCCGCACCCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTTCGCCGAGGCC 3610
Db |||||||
QY 3534 CCCACACCGAGCCCGCACCCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTTCGCCGAGGCC 3593
Db |||||||
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Db |||||||
QY 3594 TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGGCCCTGAGTGAGTGTTCGCCGAGGCC 3653
Db |||||||
QY 3671 CTGAGTGTCCAGACACACCTGCGGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCAGCC 3730
Db |||||||
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QY 3731 CAGGGCCAGCTTTTCCCTCACCAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCAT 3790
Db |||||||
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Db |||||
QY 3774 CCCAGAT 3781
Db |||||
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